

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 141.124 Seconds  
(without alignments)  
2845.805 Million cell updates/sec

Title: US-09-743-818A-5  
Perfect score: 3615  
Sequence: 1 GGVPGAIPGGVPGVYFPGA.....LSPIFGGACLGKACGRKKK 698

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3602	99.6	730	1 ELS_HUMAN	P15502 homo sapien
2	3588.5	99.3	757	2 Q14234	Q14234 homo sapien
3	3584.5	99.2	757	2 Q75MU5	Q75MU5 homo sapien
4	3584.5	99.2	757	2 AAS07435	AAS07435 homo sapi
5	3474.5	96.1	711	2 Q723F5	Q723F5 homo sapien
6	3393.5	93.9	687	2 Q14235	Q14235 homo sapien
7	3318.5	91.8	687	2 Q72316	Q72316 homo sapien
8	3200	88.5	658	2 Q6P0L4	Q6P0L4 homo sapien
9	3200	88.5	658	2 AAH65566	AAH65566 homo sapi
10	3091.5	85.5	643	2 Q8NB14	Q8NB14 homo sapien
11	2896.5	80.1	602	2 Q15337	Q15337 homo sapien
12	2870	79.4	635	2 Q15336	Q15336 homo sapien
13	2692	74.5	570	2 Q6ZM36	Q6ZM36 homo sapien
14	2692	74.5	570	2 BAC85506	BAC85506 homo sapi
15	2537	70.2	707	2 Q28098	Q28098 bos taurus
16	2505.5	69.3	747	1 ELS_BOVIN	P04985 bos taurus
17	2431	67.2	679	2 Q28097	Q28097 bos taurus
18	2388.5	66.1	860	2 Q8C918	Q8C918 mus musculus
19	2385.5	66.0	860	1 ELS_MOUSE	P54320 mus musculus
20	2315.5	64.1	864	1 ELS_RAT	Q99372 rattus norv
21	2294.5	63.5	810	2 Q8ESZ9	Q8ESZ9 mus musculus
22	2288.5	63.3	666	2 Q28096	Q28096 bos taurus
23	2240.5	62.0	650	2 Q28099	Q28099 bos taurus
24	2023.5	56.0	559	2 Q6ZUN2	Q6ZUN2 homo sapien
25	2023.5	56.0	559	2 BAC86188	BAC86188 homo sapi
26	1679	46.4	472	2 Q8N2G0	Q8N2G0 homo sapien
27	1564	43.3	750	1 ELS_CHICK	P07916 gallus gall
28	1285	35.5	258	2 Q9UMF5	Q9UMF5 homo sapien
29	797.5	22.1	172	2 Q9BDZ0	Q9BDZ0 macaca mula
30	783.5	21.7	1953	2 Q9BIT7	Q9BIT7 nephila ina
31	770	21.3	1002	2 Q9BIU8	Q9BIU8 argiope tri

ALIGNMENTS

017434	nephila cla	2	017434	988	21.1	763	32
Q7YU48	drosophila	2	Q7YU48	1071	21.1	761	33
Q9VTR6	drosophila	2	Q9VTR6	1713	21.1	761	34
Q9U617	drosophila	2	Q9U617	1729	20.9	756.5	35
Q9HW2	nephila ina	2	Q9HW2	1884	20.4	738	36
Q9HW4	nephila cla	2	Q9HW4	2249	20.2	732	37
P05790	bombyx mori	2	Q9NHW4	2249	20.0	722.5	38
Q9GUS5	galleria me	1	FB0H_BOMMO	5263	19.5	706	39
Q9BIU9	argiope tri	2	Q9GUB5	1468	19.3	697	40
Q44359	nephila cla	2	Q9BIU9	651	19.3	696	41
Q8VIZ0	mycobacteri	2	Q44359	907	19.3	696	42
Q6Q294	agelenopsis	2	Q8VIZ0	1715	19.2	695	43
AA08436	agelenops	2	Q6Q294	897	18.9	681.5	44
Q44358	nephila cla	2	AA08436	897	18.9	681.5	45
P19837	nephila cla	2	Q44358	871	18.8	679.5	46
Q5353	mycobacteri	2	SPD1_NBPCL	747	18.6	673	47
P17140	caenorhabdi	2	Q7TWG3	1460	18.6	672	48
P17163	brugia mala	2	PG54_MYCTU	1901	18.5	669.5	49
Q6PY84	kukulcania	2	CA24_CAEEL	1758	18.3	661	50
Q8VIY9	mycobacteri	2	Q17163	1802	18.2	658.5	51
Q7PT93	anopheles g	2	Q6PY84	760	18.1	653.5	52
Q964F4	antheraea y	2	Q6PY84	18.1	18.1	650	53
Q6MW6	mycobacteri	2	Q6PY84	1217	18.0	641	54
CAE55607	mycobacte	2	Q6PY84	1666	17.7	639	55
P27393	ascaris suu	2	Q6MW6	2855	17.5	632.5	56
Q76786	antheraea p	2	CAE55607	1489	17.5	632.5	57
Q7U160	mycobacteri	2	CAE55607	1763	17.5	630.5	58
Q8MW53	mytilus gal	2	CA24_ASCSU	2639	17.4	627.5	59
Q7D974	mycobacteri	2	Q7PT93	992	17.4	626.5	60
Q6J6N0	araneus ven	2	Q7U160	773	17.3	626.5	61
AA08433	kukulcani	2	Q8MW53	922	17.3	624.5	62
Q8VIY9	mycobacteri	2	Q7D974	749	17.3	624.5	63
Q7PT93	anopheles g	2	Q6J6N0	563	17.2	623	64
Q964F4	antheraea y	2	AA08433	1763	17.2	623	65
Q6MW6	mycobacteri	2	Q8VIY9	1217	17.2	622.5	66
CAE55607	mycobacte	2	Q7PT93	992	17.2	622.5	67
P27393	ascaris suu	2	Q964F4	2855	16.9	610	68
Q76786	antheraea p	2	Q6MW6	1489	16.7	605.5	69
Q7U160	mycobacteri	2	CAE55607	1763	16.7	605.5	70
Q8MW53	mytilus gal	2	CA24_ASCSU	2639	16.7	604.5	71
Q7D974	mycobacteri	2	Q7PT93	992	16.7	604.5	72
Q6J6N0	araneus ven	2	Q7U160	773	16.7	602.5	73
AA08433	kukulcani	2	Q8MW53	922	16.5	598	74
Q8VIY9	mycobacteri	2	Q6J6N0	563	16.5	597.5	75
Q7PT93	anopheles g	2	AA08433	1217	16.5	596.5	76
Q964F4	antheraea y	2	Q8VIY9	1217	16.5	595	77
Q6MW6	mycobacteri	2	Q7PT93	992	16.5	592.5	78
CAE55607	mycobacte	2	Q964F4	2855	16.4	591.5	79
P27393	ascaris suu	2	Q6MW6	1489	16.4	589.5	80
Q76786	antheraea p	2	CAE55607	1763	16.3	589.5	81
Q7U160	mycobacteri	2	CA24_ASCSU	2639	16.3	589.5	82
Q8MW53	mytilus gal	2	Q7PT93	992	16.3	589.5	83
Q7D974	mycobacteri	2	Q7U160	773	16.3	589.5	84
Q6J6N0	araneus ven	2	Q8MW53	922	16.3	589.5	85
AA08433	kukulcani	2	Q6J6N0	563	16.3	589	86
Q8VIY9	mycobacteri	2	AA08433	1217	16.3	588	87
Q7PT93	anopheles g	2	Q8VIY9	1217	16.3	588	88
Q964F4	antheraea y	2	Q7PT93	992	16.2	587.5	89
Q6MW6	mycobacteri	2	Q964F4	2855	16.2	587	90
CAE55607	mycobacte	2	Q6MW6	1489	16.2	586.5	91
P27393	ascaris suu	2	CAE55607	1763	16.2	586.5	92
Q76786	antheraea p	2	CA24_ASCSU	2639	16.2	586.5	93
Q7U160	mycobacteri	2	Q7PT93	992	16.2	585.5	94
Q8MW53	mytilus gal	2	Q7U160	773	16.2	585.5	95
Q7D974	mycobacteri	2	Q8MW53	922	16.2	585.5	96
Q6J6N0	araneus ven	2	Q6J6N0	563	16.2	585.5	97
AA08433	kukulcani	2	AA08433	1217	16.2	585.5	98
Q8VIY9	mycobacteri	2	AA08433	1217	16.1	582.5	99
Q7PT93	anopheles g	2	AA08433	1217	16.1	582.5	100





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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 31.3948 Seconds  
(without alignments)  
2139.188 Million cell updates/sec

Title: US-09-743-818A-5  
Perfect score: 3615  
Sequence: 1 GGVPAICGVPGVFGA.....LSPIPPGACLGACGRKK 698

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 79:\*

1: Pirl:  
2: Pirl:  
3: Pirl:  
4: Pirl:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3551	98.2	792	1 EAHU	elastin precursor,
2	2620	72.5	770	2 S59623	tropoelastin - she
3	2514.5	69.6	747	1 EABO	elastin precursor,
4	2385.5	66.0	860	1 EAMS	elastin precursor
5	2315.5	64.1	864	1 EART	elastin precursor
6	1718	47.5	784	2 A26601	elastin precursor
7	673	18.6	718	2 A36068	major ampullate fi
8	669.5	18.5	1901	2 F70806	hypothetical glyci
9	661	18.3	1758	2 T29350	hypothetical glyci
10	661	18.3	1759	2 T29351	hypothetical prote
11	632.5	17.5	1489	2 D70807	collagen alpha 2(I
12	632.5	17.5	1763	2 S16366	hypothetical glyci
13	630.5	17.4	2639	2 T31328	collagen alpha 2(I
14	622.5	17.2	749	2 A70812	fibroin - Chinese
15	605.5	16.7	1306	2 A70834	hypothetical glyci
16	595	16.5	1691	1 S22917	hypothetical glyci
17	589.5	16.3	778	2 F70963	collagen alpha 5(I
18	589.5	16.3	1660	2 A70869	hypothetical glyci
19	589	16.3	1882	2 B70812	hypothetical glyci
20	587	16.2	1669	1 CGHU4B	collagen alpha 1(I
21	586.5	16.2	1329	2 E70917	hypothetical glyci
22	579.5	16.0	767	2 E70895	hypothetical glyci
23	579.5	16.0	783	2 E70824	hypothetical glyci
24	577	16.0	1464	1 CGHU1S	collagen alpha 1(I
25	569.5	15.8	1669	1 CGMS4B	collagen alpha 1(I
26	566.5	15.7	1049	1 CGBO7S	collagen alpha 1(I
27	564	15.6	1042	1 CGCH1S	collagen alpha 1(I
28	564	15.6	1466	1 CGHU7L	collagen alpha 1(I
29	563	15.6	812	2 S31521	collagen COLF1 - f

30	556.5	15.4	1373	1 A43291	collagen alpha 2(I
31	556	15.4	1381	2 E70806	hypothetical glyci
32	554	15.3	1079	2 B70807	hypothetical glyci
33	553.5	15.3	914	2 H70987	hypothetical glyci
34	553.5	15.3	1418	2 D45467	collagen alpha 1(I
35	553	15.3	957	2 D70835	hypothetical glyci
36	553	15.3	1453	2 S21626	collagen alpha 1(I
37	552.5	15.3	1487	1 CGHU6C	spidroin 2, dragli
38	549	15.2	627	2 A44112	collagen alpha 1(I
39	548	15.2	1464	2 S59856	hypothetical glyci
40	546	15.1	741	2 G70917	collagen alpha 2(I
41	546	15.1	1366	1 CGHU2S	hypothetical glyci
42	545.5	15.1	853	2 A70896	hypothetical glyci
43	541	15.0	801	2 F70824	collagen alpha 2(I
44	540.5	15.0	1712	1 CGHU2B	collagen alpha 6(I
45	540	14.9	1691	1 CGHU6B	collagen alpha 1(I
46	539.5	14.9	1419	2 A41182	collagen alpha 1(I
47	539.5	14.9	1487	2 B41182	collagen alpha 1(I
48	539	14.9	1027	2 S28774	collagen alpha cha
49	539	14.9	1492	2 A40333	collagen alpha 1(I
50	532	14.7	1486	1 B40333	collagen alpha 1(I
51	530	14.7	837	2 E70835	hypothetical glyci
52	529	14.6	1538	2 H70846	hypothetical glyci
53	525.5	14.5	886	2 I50694	collagen alpha 1(I
54	524.5	14.5	1744	2 S40991	collagen alpha 2(I
55	520.5	14.4	1496	1 CGHU2V	collagen alpha 2(I
56	519.5	14.4	1707	2 A33526	collagen alpha 2(I
57	519	14.4	1497	2 I49607	procollagen type V
58	518	14.3	714	2 A70807	hypothetical glyci
59	516	14.3	779	1 CGBO1S	collagen alpha 1(I
60	508.5	14.1	694	2 F70868	hypothetical glyci
61	503.5	13.9	1690	1 CGHU1B	collagen alpha 4(I
62	501	13.9	2944	2 A54849	collagen alpha 1(V
63	500	13.8	1603	2 S23810	collagen alpha 1(X
64	496.5	13.7	1414	1 S23809	collagen alpha 2(I
65	496	13.7	603	2 A70770	hypothetical glyci
66	495.5	13.7	1806	1 CGHU1E	collagen alpha 1(X
67	493	13.6	1546	1 CGHU2E	collagen alpha 2(X
68	493	13.6	1670	1 CGHU3B	collagen alpha 3(I
69	492	13.6	1752	2 A45407	collagen alpha 3(I
70	488.5	13.5	923	2 E70820	hypothetical glyci
71	486.5	13.5	408	2 S57483	glycin-rich protei
72	486.5	13.5	635	2 A57131	collagen alpha 2(V
73	486.5	13.5	671	1 CGRT1S	collagen alpha 1(I
74	485.5	13.4	1775	2 A31893	collagen alpha 1(I
75	485	13.4	1747	2 A54121	collagen alpha-4 c
76	483.5	13.4	754	2 A55267	collagen alpha 5(I
77	482	13.3	964	1 CGCH2S	collagen alpha 2(I
78	481.5	13.3	677	2 S23296	collagen alpha 2(I
79	480.5	13.3	618	2 A70989	hypothetical glyci
80	478.5	13.2	744	2 S15435	collagen alpha 1(V
81	478	13.2	744	1 A34246	collagen alpha 1(V
82	478	13.2	744	1 S23298	collagen alpha 1(V
83	477	13.2	1843	2 S18803	collagen alpha 1(V
84	476.5	13.2	743	1 S23779	collagen alpha 1(X
85	476	13.2	680	1 CGHU1D	collagen alpha 1(V
86	474	13.1	1838	1 CGHU1V	collagen alpha 1(X
87	472.5	13.1	1142	2 JX0369	hypothetical glyci
88	471.5	13.0	731	2 C70974	hypothetical glyci
89	467	12.9	1011	2 F70620	collagen alpha 1(X
90	467	12.9	1024	2 S18251	collagen alpha 1(X
91	466.5	12.9	1549	2 I48103	type VII collagen
92	465.5	12.9	584	2 G70804	hypothetical glyci
93	465	12.9	3198	2 A43426	collagen alpha 2 f
94	463	12.8	469	2 A24450	collagen alpha 1(I
95	463	12.8	920	2 B34493	collagen alpha 1(I
96	459.5	12.7	667	2 A70893	hypothetical glyci
97	458.5	12.7	1958	2 B40505	hypothetical prote
98	456	12.6	606	2 H70816	hypothetical glyci
99	455	12.6	920	2 A45748	collagen alpha 1(V
100	449.5	12.4	591	2 B70523	hypothetical glyci

## ALIGNMENTS

## RESULT 1

EHU  
 elastin precursor, long splice form - human  
 N:Alternate names: tropoelastin  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Jun-1990 #sequence revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: A32707; A33705; A30524; A53891  
 R:Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987  
 A:Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA  
 A:Reference number: A32707; MUID:87289668; PMID:3039501  
 A:Accession: A32707  
 A:Molecule type: mRNA  
 A:Residues: 1-500,507-792 <IND>  
 A:Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948  
 R:Bashtir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.  
 J. Biol. Chem. 264, 8887-8891, 1989  
 A:Title: Characterization of the complete human elastin gene. Delineation of unusual features  
 A:Reference number: A33705; MUID:89255358; PMID:2722804  
 A:Accession: A33705  
 A:Molecule type: DNA  
 A:Residues: 1-27 <BAS>  
 A:Cross-references: GB:J04821; NID:g182052; PIDN:AAA52379.1; PID:g553276  
 R:Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.  
 J. Invest. Dermatol. 91, 458-464, 1988  
 A:Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA  
 A:Reference number: A30524; MUID:89009960; PMID:3171221  
 A:Accession: A30524  
 A:Molecule type: mRNA  
 A:Residues: 1-453,483-617,651-792 <PAZ>  
 A:Cross-references: ENBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062  
 A:Note: this sequence represents a composite of several splice forms  
 R:Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U  
 Lab. Invest. 58, 270-277, 1988  
 A:Title: Isolation and characterization of human elastin cDNAs, and age-associated variations  
 A:Reference number: A53891; MUID:88156138; PMID:2831431  
 A:Accession: A53891  
 A:Molecule type: mRNA  
 A:Residues: 164-453,483-500,507-617,651-792 <PAZ>  
 A:Cross-references: GB:M24782; NID:g182063; PIDN:AAA53190.1; PID:g182064  
 C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix  
 C:Genetics:  
 A:Gene: GDB:ELN  
 A:Cross-references: GDB:119107; OMIM:130160  
 A:Map position: 7q11.23-7q11.23  
 C:Superfamily: elastin  
 C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-792/Product: elastin #status predicted <MAT>  
 F:782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;  
 Best Local Similarity 91.1%; Pred. No. 6.2e-154;  
 Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGVPGGVYFPGAGLGGALGPGGKPLKPVPGGLAGAGLGAAGLGAFFAVT 60  
 DB 27 GGVPGAI PGVPGGVYFPGAGLGGALGPGGKPLKPVPGGLAGAGLGAAGLGAFFAVT 86  
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSGAGAVVPPGAGVPGKVPVGGV 120  
 DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSGAGAVVPPGAGVPGKVPVGGV 146  
 QY 121 PGVYPGGVLPGARFPGVGLPVGPTGAGVKPKAFGVGGAFAGIFGVGFGFGPQGPVPLGY 180  
 DB 147 PGVYPGGVLPGARFPGVGLPVGPTGAGVKPKAFGVGGAFAGIFGVGFGFGPQGPVPLGY 206  
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240

DB 207 PIKAPKLPGGYGLPYTTGKLPYGVPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 266  
 QY 241 GAGAGVLPFGVGAGVPGVPGAIPIGGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 300  
 DB 267 GAGAGVLPFGVGAGVPGVPGAIPIGGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 326  
 QY 301 PGFPGVPGVPGAGVPGVPGAGIPVVPAGAGIPGAAGVPGVSPAAAAAATAAKAAYGAR 360  
 DB 327 PGFPGVPGVPGAGVPGVPGAGIPVVPAGAGIPGAAGVPGVSPAAAAAATAAKAAYGAR 386  
 QY 361 PGVGVGGIPTYGVGAGGFFGFGVGGIPGVAGVPGVPGVGGVPGVGGISPEAQAAAA 420  
 DB 387 PGVGVGGIPTYGVGAGGFFGFGVGGIPGVAGVPGVPGVGGVPGVGGISPEAQAAAA 446  
 QY 421 AKAAKY-----GVGTAAAAAATAAKAAYG----- 445  
 DB 447 AKAAKYAAGAGAGVGLGVLPGPQAAVPGVGTGGVPGVGTAAAAAATAAKAAYG----- 506  
 QY 446 GLVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 505  
 DB 507 GLVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 566  
 QY 506 AKVAAKAOIRAAAGLCAAGIPGLGVGVPGLGVGAGVPGVPGVPGVPGVPGVPGVPGV 556  
 DB 567 AKVAAKAOIRAAAGLCAAGIPGLGVGVPGLGVGAGVPGVPGVPGVPGVPGVPGVPGV 626  
 QY 557 -----VPGALAAATAAKAAYGAAVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 592  
 DB 627 LSPELREGDPSSSHLPSTSPRVPAGALAAATAAKAAYGAAVPGVPGVPGVPGVPGVPGV 686  
 QY 593 VGAGPAAAAATAAKAAYGAAVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 652  
 DB 687 VGAGPAAAAATAAKAAYGAAVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 746  
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RESULT 2  
 SS9623  
 tropoelastin - sheep  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C>Date: 23-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C:Accession: SS9623; A24758  
 R:Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; B  
 Matrix Biol. 14, 635-641, 1994  
 A:Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.  
 A:Reference number: SS9623  
 A:Accession: SS9623  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-770 <MAU>  
 A:Cross-references: UNIPROT:P11547  
 R:Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smi  
 Arch. Biochem. Biophys. 241, 684-691, 1985  
 A:Title: Analysis of the 3' region of the sheep elastin gene.  
 A:Reference number: A24758; MUID:85305763; PMID:3839997  
 A:Accession: A24758  
 A:Molecule type: mRNA  
 A:Residues: 655-669,671-716,732-770 <YOO>  
 C:Superfamily: elastin  
 C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
 F:760-765/Disulfide bonds: #status predicted

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 Best Local Similarity 70.7%; Pred. No. 7e-112;  
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 DB 27 GGVLGVPGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 86

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:37:11 ; Search time 113.997 Seconds  
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Perfect score: 3615  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1570615

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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  - 20: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3366	93.1	692	15	US-10-210-172-40
5	3233.5	89.4	663	15	US-10-108-260A-2477
6	2951.5	81.6	617	14	US-10-104-047-2915
7	1155	32.0	988	8	US-08-806-029-28
8	1154	31.9	965	16	US-10-800-179-31
9	1150.5	31.8	832	8	US-08-806-029-27
10	1139.5	31.5	936	8	US-08-806-029-26
11	1139.5	31.5	1038	16	US-10-800-179-30
12	1133	31.3	745	9	US-09-837-969A-38
13	1133	31.3	745	9	US-09-841-321A-38
Sequence 8, Appli					
Sequence 1, Appli					
Sequence 38, Appl					
Sequence 40, Appl					
Sequence 2477, Ap					
Sequence 2915, Ap					
Sequence 28, Appl					
Sequence 31, Appl					
Sequence 27, Appl					
Sequence 26, Appl					
Sequence 30, Appl					
Sequence 38, Appl					
Sequence 38, Appl					

14	1131.5	31.3	1002	14	US-10-117-931-25	Sequence 25, Appl
15	1131	31.3	889	14	US-08-806-029-19	Sequence 19, Appl
16	1129.5	31.2	1465	14	US-10-096-986-74	Sequence 74, Appl
17	1125.5	31.1	884	14	US-10-117-931-15	Sequence 15, Appl
18	1122.5	31.1	1056	8	US-08-806-029-29	Sequence 29, Appl
19	1115.5	30.9	768	8	US-08-806-029-35	Sequence 35, Appl
20	1109.5	30.7	972	8	US-08-806-029-30	Sequence 30, Appl
21	1109	30.7	884	16	US-10-800-179-25	Sequence 25, Appl
22	1108.5	30.7	2257	14	US-10-096-986-82	Sequence 82, Appl
23	1093.5	30.2	936	14	US-10-117-931-30	Sequence 30, Appl
24	1092	30.2	1040	8	US-08-806-029-32	Sequence 32, Appl
25	1091.5	30.2	696	15	US-10-441-965-23	Sequence 23, Appl
26	1091.5	30.2	696	15	US-08-806-029-25	Sequence 25, Appl
27	1091.5	30.2	750	8	US-08-806-029-14	Sequence 14, Appl
28	1082	29.9	953	8	US-08-806-029-25	Sequence 21, Appl
29	1080	29.9	696	15	US-10-441-965-21	Sequence 31, Appl
30	1080	29.9	1024	8	US-08-806-029-31	Sequence 81, Appl
31	1074	29.7	2055	14	US-10-096-986-81	Sequence 34, Appl
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37	1009.5	27.9	2003	9	US-09-837-969A-34	Sequence 34, Appl
38	1009.5	27.9	2003	9	US-09-841-321A-34	Sequence 35, Appl
39	1006.5	27.8	1085	9	US-09-837-969A-35	Sequence 35, Appl
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44	990	27.4	1255	9	US-09-841-321A-18	Sequence 39, Appl
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46	989.5	27.4	1085	9	US-09-841-321A-39	Sequence 59, Appl
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54	977.5	27.0	1210	16	US-10-720-025-25	Sequence 40, Appl
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56	975	27.0	605	14	US-09-841-321A-40	Sequence 62, Appl
57	975	27.0	605	14	US-10-356-088-62	Sequence 80, Appl
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59	958.5	26.5	1300	9	US-09-837-969A-55	Sequence 55, Appl
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62	947.5	26.2	635	9	US-09-837-969A-36	Sequence 25, Appl
63	947.5	26.2	635	9	US-09-841-321A-25	Sequence 36, Appl
64	947.5	26.2	635	9	US-09-841-321A-25	Sequence 94, Appl
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68	913	25.3	1169	8	US-08-806-029-33	Sequence 38, Appl
69	912.5	25.2	485	16	US-10-720-025-21	Sequence 6, Appl
70	911	25.2	475	16	US-10-720-025-38	Sequence 54, Appl
71	901	24.9	450	9	US-09-812-382-6	Sequence 60, Appl
72	885.5	24.5	1536	17	US-10-479-638-54	Sequence 54, Appl
73	849	23.5	1382	16	US-10-720-025-60	Sequence 35, Appl
74	849	23.5	1550	16	US-10-720-025-54	Sequence 35, Appl
75	833	23.0	730	16	US-10-720-025-35	Sequence 53, Appl
76	766.5	21.2	562	16	US-10-720-025-33	Sequence 53, Appl
77	753.5	20.8	2304	17	US-10-479-638-53	Sequence 52, Appl
78	744	20.6	528	16	US-10-720-025-43	Sequence 51, Appl
79	734	20.3	2016	17	US-10-479-638-52	Sequence 26, Appl
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87 701.5 19.4 1617 14 US-10-414-760-14 Sequence 14, Appl  
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 89 692.5 19.2 312 8 US-08-806-029-34 Sequence 34, Appl  
 90 690 19.1 809 14 US-10-414-760-13 Sequence 13, Appl  
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 92 674.5 18.7 1130 16 US-10-720-025-61 Sequence 61, Appl  
 93 672 18.6 651 9 US-09-861-597-1 Sequence 1, Appl  
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 95 671.5 18.6 979 14 US-10-096-986-99 Sequence 89, Appl  
 96 670 18.5 780 15 US-10-441-985-25 Sequence 25, Appl  
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 98 664 18.4 766 14 US-10-096-986-88 Sequence 88, Appl  
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## ALIGNMENTS

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 ; Sequence 8, Application US/09961403  
 ; Publication No. US2003007589A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HE-STUMPP, HOLGER  
 ; APPLICANT: HAENDLER, BERNARD  
 ; APPLICANT: KRAETZSCHMAR, JOERN  
 ; APPLICANT: KREFT, BERTHOLT  
 ; APPLICANT: WINTERHAGER, ELKE  
 ; APPLICANT: REGIDOR, PEDRO  
 ; APPLICANT: SCOTTI, SIMONE  
 ; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS  
 ; FILE REFERENCE: SCH-1789  
 ; CURRENT APPLICATION NUMBER: US/09/961,403  
 ; CURRENT FILING DATE: 2001-09-25  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 730  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-961-403-8

Query Match 99.6%; Score 3602; DB 10; Length 730;  
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US-09-964-662-1  
 ; Sequence 1, Application US/09964662  
 ; Publication No. US20030166846A1  
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 ; APPLICANT: PROTEIN SPECIALTIES LTD.  
 ; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP  
 ; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND  
 ; TITLE OF INVENTION: OTHER FIBROUS PROTEINS  
 ; FILE REFERENCE: 041082/0112  
 ; CURRENT APPLICATION NUMBER: US/09/964,662  
 ; CURRENT FILING DATE: 2003-05-08  
 ; PRIOR APPLICATION NUMBER: 09/340,736  
 ; PRIOR FILING DATE: 1999-06-29  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 731  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-964-662-1

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OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1570615

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Listing first 100 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3261	95.2	730	10	US-09-961-403-8
2	3237.5	94.5	731	10	US-09-964-662-1
3	3145.5	91.8	711	15	US-10-210-172-38
4	3042	88.8	692	15	US-10-210-172-40
5	3025.5	88.3	663	15	US-10-108-260A-2477
6	2679.5	78.2	617	14	US-10-104-047-2915
7	1096	32.0	988	8	US-08-806-029-28
8	1087.5	31.7	745	9	US-09-837-969A-38
9	1087.5	31.7	745	9	US-09-841-321A-38
10	1086.5	31.7	832	8	US-08-806-029-27
11	1076.5	31.4	1056	8	US-08-806-029-29
12	1076	31.4	965	16	US-10-800-179-31
13	1069.5	31.2	2257	14	US-10-096-986-82
					Sequence 8, Appl
					Sequence 1, Appl
					Sequence 38, Appl
					Sequence 40, Appl
					Sequence 2477, Ap
					Sequence 2915, Ap
					Sequence 28, Appl
					Sequence 38, Appl
					Sequence 36, Appl
					Sequence 27, Appl
					Sequence 29, Appl
					Sequence 31, Appl
					Sequence 82, Appl

Sequence 19, Appl  
Sequence 15, Appl  
Sequence 30, Appl  
Sequence 26, Appl  
Sequence 30, Appl  
Sequence 35, Appl  
Sequence 74, Appl  
Sequence 25, Appl  
Sequence 25, Appl  
Sequence 36, Appl  
Sequence 23, Appl  
Sequence 25, Appl  
Sequence 31, Appl  
Sequence 21, Appl  
Sequence 14, Appl  
Sequence 81, Appl  
Sequence 32, Appl  
Sequence 30, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 34, Appl  
Sequence 80, Appl  
Sequence 37, Appl  
Sequence 37, Appl  
Sequence 34, Appl  
Sequence 34, Appl  
Sequence 35, Appl  
Sequence 35, Appl  
Sequence 77, Appl  
Sequence 1, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 39, Appl  
Sequence 39, Appl  
Sequence 40, Appl  
Sequence 40, Appl  
Sequence 62, Appl  
Sequence 52, Appl  
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Sequence 59, Appl  
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Sequence 25, Appl  
Sequence 36, Appl  
Sequence 41, Appl  
Sequence 23, Appl  
Sequence 24, Appl  
Sequence 42, Appl  
Sequence 25, Appl  
Sequence 94, Appl  
Sequence 62, Appl  
Sequence 33, Appl  
Sequence 6, Appl  
Sequence 21, Appl  
Sequence 55, Appl  
Sequence 55, Appl  
Sequence 38, Appl  
Sequence 35, Appl  
Sequence 54, Appl  
Sequence 53, Appl  
Sequence 33, Appl  
Sequence 43, Appl  
Sequence 2, Appl  
Sequence 9, Appl  
Sequence 64, Appl  
Sequence 11, Appl  
Sequence 26, Appl  
Sequence 34, Appl  
Sequence 14, Appl  
Sequence 24, Appl



	QY	2	GGVPGAVPGVGGVYFPGAGFGA	25
Db	27	GGVPGAI	PGVPGVYFPGAGLGGGALPGGKPLKVPVGGLAGAGLGAFAFPAVT	86
QY	26	-----	VPGGVADAAAAYKAAKAGAGLGGVPGVGGIGVTSAGAVVPPQGNKVPKVPVGL	80
Db	87	FPGALV	FGGVADAAAAYKAAKAGAGLGGVPGVGGIGVTSAGAVVPPQGNKVPKVPVGL	146
QY	81	PGVYFG	FAGVPGVGVLPVPTGAGVKPKAPGVGGAFAGIPGVPGPGPGVPLG	140
Db	147	PGVYFG--	GVLPGAREPFGVLPVPGVTGAGVKPKAPGVGGAFAGIPGVPGPGPGVPLG	205
QY	141	YPIKAP	KLPGGYGLPYTTGKLPYGVPGGVGAAGKAGYPTGTCVGPQAAAAAATAKAAK	200
Db	206	YPIKAP	KLPGGYGLPYTTGKLPYGVPGGVGAAGKAGYPTGTCVGPQAAAAAATAKAAK	265
QY	201	FGAAG	FAGVPGVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAKAAKAGAAAGLV	260
Db	266	FGAGAA--	GVLPGVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAKAAKAGAAAGLV	323
QY	261	PGGPG	FGGVPGFAGVPGVPGAGIPVVPAGIPGAAGFAGVSPAAAAKAAKAAK	320
Db	324	PGGPG	FGGVPGFAG--VPGVGPVPGAGIPVVPAGIPGAAGVPGVSPAAAAKAAKAAK	382
QY	321	YGARP	GVGGIPTYGVGAGGFPFGVGGVIGIPVAGVPSVGGVPGVGGVPGVIGISPQAQ	380



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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 29.7306 Seconds  
(without alignment)  
2139.188 Million cell updates/sec

Title: US-09-743-818A-6  
Perfect score: 3426  
Sequence: 1 MGVPGAVPGVGGVYFPG.....LSPIFFGGACLGKACGRKK 661

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 79:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3210	93.7	792	1 EAHU	elastin precursor,
2	2413	70.4	770	2 S59623	tropoelastin - she
3	2322.5	67.8	747	1 EABO	elastin precursor,
4	2162.5	63.1	860	1 EAMS	elastin precursor
5	2153.5	62.9	864	1 EART	elastin precursor
6	1587	46.3	784	2 A26601	elastin precursor
7	656.5	19.2	1901	2 F70806	hypothetical glyci
8	655	19.1	2639	2 T31328	fibroin - Chinese
9	645	18.8	1758	2 T29350	hypothetical prote
10	645	18.8	1759	2 T29351	collagen alpha 2(I
11	640.5	18.7	718	2 A36068	major amputate fi
12	617	18.0	1489	2 D70807	hypothetical glyci
13	609.5	17.8	1763	2 S16366	collagen alpha 2(I
14	592.5	17.3	1306	2 A70934	hypothetical glyci
15	587.5	17.1	778	2 F70963	hypothetical glyci
16	583	17.0	1660	2 A70869	hypothetical glyci
17	577.5	16.9	1669	1 CGHU4B	collagen alpha 1(I
18	577	16.8	1691	1 S22917	collagen alpha 5(I
19	576	16.8	1329	2 E70917	hypothetical glyci
20	572	16.7	882	2 E70812	hypothetical glyci
21	570.5	16.7	749	2 E70895	hypothetical glyci
22	570	16.6	767	2 E70824	hypothetical glyci
23	567.5	16.6	783	2 E70824	hypothetical glyci
24	558	16.3	1669	1 CGMS4B	collagen alpha 1(I
25	552	16.1	1042	1 CGCH1S	collagen alpha 1(I
26	548.5	16.0	1373	1 A43291	collagen alpha 2(I
27	546.5	16.0	1464	1 CGHU1S	collagen alpha 1(I
28	546	15.9	1049	1 CGBO7S	collagen alpha 1(I
29	545	15.9	1466	1 CGHU7L	collagen alpha 1(I

30	541	15.8	1381	2 E70806	hypothetical glyci
31	538	15.7	1418	2 T45467	collagen alpha 1(I
32	537.5	15.7	1079	2 B70807	hypothetical glyci
33	535	15.6	957	2 D70835	hypothetical glyci
34	534.5	15.6	812	2 S31521	collagen COL1 - f
35	534	15.6	1464	2 S59856	collagen alpha 1(I
36	534	15.6	1487	1 CGHU6C	collagen alpha 1(I
37	533	15.6	741	2 G70917	hypothetical glyci
38	532	15.5	1691	1 CGHU6B	collagen alpha 6(I
39	528	15.4	1027	2 S28774	collagen alpha cha
40	527.5	15.4	627	2 A44112	spidrin 2, dragli
41	527.5	15.4	914	2 A70987	hypothetical glyci
42	524	15.3	853	2 A70896	hypothetical glyci
43	523.5	15.3	1453	2 S21626	collagen alpha 1(I
44	523.5	15.3	1492	2 A40333	collagen alpha 1(I
45	523	15.3	1419	2 A41182	collagen alpha 1(I
46	523	15.3	1487	2 B41182	collagen alpha 1(I
47	521	15.2	1486	1 B40333	collagen alpha 1(I
48	519.5	15.2	1366	1 CGHU2S	collagen alpha 2(I
49	516.5	15.1	1707	2 A33526	collagen alpha 2(I
50	516	15.1	1538	2 H70846	hypothetical glyci
51	514.5	15.0	801	2 F70824	hypothetical glyci
52	514	15.0	1712	1 CGHU2B	collagen alpha 1(I
53	514	15.0	2944	2 A54849	collagen alpha 1(I
54	512	14.9	1744	2 S40991	collagen alpha 1(I
55	511	14.9	886	2 I50694	hypothetical glyci
56	510.5	14.9	694	2 F70868	hypothetical glyci
57	508.5	14.8	1497	2 I49607	collagen type V
58	508	14.8	779	1 CGBO1S	collagen alpha 1(I
59	505	14.7	837	2 E70835	hypothetical glyci
60	498	14.5	1603	2 S23810	collagen alpha 1(X
61	497	14.5	714	2 A70807	hypothetical glyci
62	494	14.4	408	2 S57483	glycin-rich protei
63	493	14.4	1496	1 CGHU2V	collagen alpha 2(V
64	492.5	14.4	744	1 A34246	collagen alpha 1(V
65	492.5	14.4	744	1 S23298	collagen alpha 1(V
66	492.5	14.4	744	2 S15435	collagen alpha 2(V
67	491	14.3	635	2 A57131	collagen alpha 3(I
68	490.5	14.3	1670	1 CGHU3B	collagen alpha 1(I
69	489	14.3	671	1 CGRT1S	collagen alpha 3(I
70	485.5	14.2	1752	2 A45407	hypothetical glyci
71	485	14.2	618	2 A70989	collagen alpha 4(I
72	485	14.2	1690	1 CGHU1B	hypothetical glyci
73	483.5	14.1	603	2 A70770	hypothetical glyci
74	482.5	14.1	923	2 E70820	hypothetical glyci
75	481.5	14.1	743	1 S23779	collagen alpha 1(V
76	479	14.0	1414	1 S23609	collagen alpha 2(I
77	478.5	14.0	1549	2 I48103	type VII collagen
78	476.5	13.9	964	1 CGCH2S	collagen alpha 2(I
79	476.5	13.9	1747	2 A54121	collagen alpha 4 c
80	474.5	13.8	469	2 A24450	collagen alpha 2(V
81	474	13.8	1546	1 CGHU2E	collagen alpha 2(X
82	473.5	13.8	754	2 A55267	collagen alpha 5(I
83	469.5	13.7	677	2 S23296	collagen alpha 2(I
84	469	13.7	1806	1 CGHU1E	collagen alpha 1(X
85	468	13.7	680	1 CGHU1D	collagen alpha 1(X
86	467.5	13.6	1775	2 A31893	hypothetical glyci
87	463	13.5	667	2 A70893	collagen alpha 2 f
88	462	13.5	3198	2 A43426	hypothetical glyci
89	461.5	13.5	606	2 H70816	hypothetical glyci
90	461.5	13.5	688	2 A53330	hypothetical glyci
91	461.5	13.5	731	2 G70974	glycine-rich prote
92	461.5	13.4	584	2 G70804	hypothetical glyci
93	453.5	13.2	608	2 T05442	collagen alpha 1(X
94	453	13.2	1011	2 F70620	hypothetical glyci
95	453	13.2	1024	2 S18251	hypothetical glyci
96	452.5	13.2	591	2 B70523	collagen alpha 1(X
97	451.5	13.2	674	2 S13301	collagen alpha 1(I
98	446	13.0	920	2 B34493	collagen alpha 1(I
99	444	13.0	921	2 S42617	collagen alpha 1(I
100	443.5	12.9	1843	2 S18803	collagen alpha 1(V



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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 133.643 Seconds  
(without alignments)  
2845.805 Million cell updates/sec

Title: US-09-743-818A-6

Perfect score: 3426

Sequence: 1 MGVPVCAVPGVGVFGVPG.....LSPIFGGACLGKACGRKEK 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3261	95.2	730	1	ELS_HUMAN
2	3247.5	94.8	757	2	Q14234
3	3243.5	94.7	757	2	Q75MD5
4	3243.5	94.7	757	2	AAS07435
5	3133.5	91.5	711	2	Q723F5
6	3052.5	89.1	687	2	Q14235
7	3039.5	88.7	687	2	Q72316
8	2859	83.5	658	2	Q6P0L4
9	2859	83.5	658	2	AAR65566
10	2833.5	82.7	643	2	Q8NB14
11	2570	75.0	602	2	O15337
12	2543.5	74.2	635	2	O15336
13	2533	73.9	570	2	Q6ZMJ6
14	2533	73.9	570	2	BAC85506
15	2366.5	69.1	707	2	Q28098
16	2313.5	67.5	747	1	ELS_BOVIN
17	2270.5	66.3	679	2	Q28097
18	2165.5	63.2	860	2	Q8C9L8
19	2162.5	63.1	860	1	ELS_MOUSE
20	2153.5	62.9	864	1	ELS_RAT
21	2132.5	62.2	810	2	Q9ES29
22	2118	61.8	666	2	Q28096
23	2070	60.4	650	2	Q28099
24	1759	51.3	559	2	Q6ZUN2
25	1759	51.3	559	2	BAC86188
26	1531	44.7	472	2	Q8N2G0
27	1433	41.8	750	1	ELS_CHICK
28	1270.5	37.1	258	2	Q9UMF5
29	790	23.1	1071	2	Q7YU48
30	790	23.1	1713	2	Q9VTR6
31	775.5	22.6	1729	2	Q9U617

32	763.5	22.3	988	2	O17434	O17434	nephila cla
33	727.5	21.2	1002	2	Q9BIU8	Q9BIU8	argiope tri
34	724.5	21.1	5263	1	FB0H_BOMMO	FB0H_BOMMO	bombyx mori
35	716	20.9	1953	2	Q9BIT7	Q9BIT7	nephila ina
36	678	19.8	897	2	Q6Q294	Q6Q294	agelenopsis
37	678	19.8	897	2	AAT08436	AAT08436	agelenopsis
38	676.5	19.7	1884	2	Q9NHW2	Q9NHW2	nephila ina
39	674.5	19.7	651	2	Q9BIU9	Q9BIU9	argiope tri
40	663	19.4	1468	2	Q9GUB5	Q9GUB5	galleria me
41	661	19.3	1715	2	Q8VIZ0	Q8VIZ0	mycobacteri
42	660.5	19.3	2249	2	Q9NHW4	Q9NHW4	nephila cla
43	656.5	19.2	1901	1	PG54_MYCTU	PG54_MYCTU	mycobacteri
44	656.5	19.2	2655	2	Q964F4	Q964F4	antheraea y
45	655	19.1	2639	2	Q76786	Q76786	antheraea p
46	651.5	19.0	172	2	Q9BDZ0	Q9BDZ0	macaca mula
47	651.5	19.0	1460	2	Q7TWC3	Q7TWC3	mycobacteri
48	650	19.0	760	2	Q6PY84	Q6PY84	kukulcania
49	650	19.0	760	2	AAT08433	AAT08433	kukulcania
50	645.5	18.8	871	2	O44358	O44358	nephila cla
51	645	18.8	1758	1	CA24_CAEEL	CA24_CAEEL	caenorhabdi
52	640.5	18.7	747	1	SPD1_NEPCL	SPD1_NEPCL	nephila cla
53	631	18.4	1666	2	Q7PT93	Q7PT93	anopheles g
54	625	18.2	1802	2	Q17163	Q17163	brugia mala
55	621.5	18.1	907	2	O44359	O44359	nephila cla
56	617	18.0	1489	2	Q6MWW6	Q6MWW6	mycobacteri
57	617	18.0	1489	2	CAE55607	CAE55607	mycobacte
58	615.5	18.0	992	2	Q7TWB8	Q7TWB8	mycobacteri
59	611	17.8	922	2	Q8MW53	Q8MW53	mytilus gal
60	609.5	17.8	1763	1	CA24_ASCSU	CA24_ASCSU	ascaris suu
61	609	17.7	1217	2	Q8V1Y9	Q8V1Y9	mycobacteri
62	606	17.7	691	2	Q9BIU3	Q9BIU3	dolomedes t
63	602.5	17.6	617	2	O46172	O46172	nephila cla
64	599.5	17.5	922	2	O44367	O44367	mytilus edu
65	594	17.3	644	2	Q8WSM4	Q8WSM4	nephila cla
66	592.5	17.3	1306	2	Q7D9L6	Q7D9L6	mycobacteri
67	592.5	17.3	1306	2	Q7UIQ7	Q7UIQ7	mycobacteri
68	592.5	17.3	1306	2	Q6MX28	Q6MX28	mycobacteri
69	592.5	17.3	1306	2	CAE55300	CAE55300	mycobacte
70	589	17.2	563	2	Q6J6N0	Q6J6N0	araneus ven
71	589	17.2	563	2	AAT36347	AAT36347	araneus v
72	587.5	17.1	778	1	PG46_MYCTU	PG46_MYCTU	mycobacteri
73	583	17.0	1660	2	Q79FD4	Q79FD4	mycobacteri
74	583	17.0	1660	2	CAE55496	CAE55496	mycobacte
75	583	17.0	1665	2	Q7D721	Q7D721	mycobacteri
76	582.5	17.0	774	2	Q7U0P7	Q7U0P7	mycobacteri
77	582.5	17.0	854	2	Q9BIU4	Q9BIU4	dolomedes t
78	580.5	16.9	1691	2	Q9ESQ2	Q9ESQ2	mus muscucu
79	578.5	16.9	783	2	Q7D9C6	Q7D9C6	mycobacteri
80	577.5	16.9	1669	1	CA14_HUMAN	CA14_HUMAN	homo sapien
81	577	16.8	648	2	Q9BIU7	Q9BIU7	argiope tri
82	577	16.8	1685	1	CA54_HUMAN	CA54_HUMAN	homo sapien
83	576.5	16.8	1408	2	Q8VK17	Q8VK17	mycobacteri
84	576	16.8	1329	2	Q79FP2	Q79FP2	mycobacteri
85	576	16.8	1329	2	CAE55390	CAE55390	mycobacte
86	575	16.8	773	2	Q7UI60	Q7UI60	mycobacteri
87	575	16.8	1621	2	Q9H4R9	Q9H4R9	homo sapien
88	574.5	16.8	1408	2	Q7U022	Q7U022	mycobacteri
89	574	16.8	1075	2	Q86X41	Q86X41	homo sapien
90	572.5	16.7	749	2	Q7D974	Q7D974	mycobacteri
91	572.5	16.7	879	2	Q8VKD2	Q8VKD2	mycobacteri
92	572	16.7	882	2	Q79FV6	Q79FV6	mycobacteri
93	572	16.7	882	2	CAE55329	CAE55329	mycobacte
94	571.5	16.7	797	2	Q7UID4	Q7UID4	mycobacteri
95	571	16.7	626	2	Q9NHW1	Q9NHW1	nephila ina
96	570.5	16.7	749	2	Q79FV7	Q79FV7	mycobacteri
97	570.5	16.7	749	2	CAE55328	CAE55328	mycobacte
98	570	16.6	767	2	Q79FT0	Q79FT0	mycobacteri
99	570	16.6	767	2	CAE55354	CAE55354	mycobacte
100	569	16.6	831	2	Q7UI59	Q7UI59	mycobacteri

ALIGNMENTS



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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 0.584716 Seconds  
(without alignments)  
2139.188 Million cell updates/sec

Title: US-09-743-818A-13

Perfect score: 59

Sequence: 1 ALARAKAAKYGAA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	792	1 EAHU	elastin precursor,
2	54	91.5	770	2 S59623	tropoelastin - sne
3	53	89.8	860	1 EAMS	elastin precursor
4	53	89.8	864	1 EART	elastin precursor
5	50	84.7	747	1 EABO	elastin precursor,
6	50	84.7	784	2 A26601	elastin precursor,
7	43	72.9	382	2 AH2361	endo-1,4-beta-xyla
8	40	67.8	375	2 AH3110	oxoreductase [limpo
9	40	67.8	375	2 D98176	hypothetical prote
10	39	66.1	253	2 A97052	probable lytic mur
11	39	66.1	336	2 D42653	dihydrolipoamide d
12	39	66.1	485	2 F87448	succinylglutamic s
13	38	64.4	704	2 A34337	propionyl-CoA carb
14	38	64.4	860	2 F71000	hypothetical prote
15	37	62.7	183	2 S33422	hypothetical prote
16	37	62.7	244	2 F95262	hypothetical prote
17	37	62.7	252	1 E36914	molybdate-binding
18	37	62.7	285	2 G75468	hypothetical prote
19	37	62.7	320	2 S05208	chorion protein s3
20	37	62.7	335	2 E71201	probable glucose-f
21	37	62.7	388	2 D91240	probable amino aci
22	37	62.7	388	2 A86088	probable hippurica
23	37	62.7	439	2 G70693	probable dinF prot
24	37	62.7	452	2 C83998	acetyl-CoA carboxy
25	37	62.7	453	2 E95367	probable methyltra
26	37	62.7	462	2 T36807	probable aldehyde
27	37	62.7	514	1 QJMWPB	photosystem II chl
28	37	62.7	524	2 T39993	N2,N2-dimethylguan
29	37	62.7	548	2 T46565	tRNA (guanine-N2-)

30	62.7	902	2 A86926	probable membrane
31	62.7	920	2 C70668	probable mmpL7 pro
32	61.0	115	2 C64160	hypothetical prote
33	61.0	154	2 T00556	60S ribosomal prot
34	61.0	251	2 A87651	conserved hypotet
35	61.0	269	2 B82335	MutT/nudix family
36	61.0	295	2 A81318	probable lipid A b
37	61.0	322	2 E95995	probable sugar upt
38	61.0	325	2 G87344	alcohol dehydrogen
39	61.0	355	2 A2867	endo-1,4-beta-xyla
40	61.0	359	2 T44816	brp protein [impor
41	61.0	365	2 E97644	endo-1,4-beta-xyla
42	61.0	368	2 F84300	bacteriorhodopsin
43	61.0	607	2 S70106	probable arginine-
44	61.0	732	2 A43315	ETS domain protein
45	61.0	766	2 H81794	ATP-dependent DNA
46	61.0	766	2 G81216	ATP-dependent DNA
47	61.0	794	2 T40289	hypothetical prote
48	61.0	860	2 T14650	tail fiber protein
49	61.0	978	2 T14968	phage lambda-relat
50	61.0	1194	2 D49851	magnesium-protopor
51	59.3	113	2 T36789	hypothetical prote
52	59.3	122	2 C95157	ribosomal protein
53	59.3	127	2 B98023	50S ribosomal prot
54	59.3	184	2 H84780	probable Ap2 domai
55	59.3	251	2 B82839	3-oxoacyl-[ACP] re
56	59.3	252	2 G87289	hypothetical prote
57	59.3	268	2 H82757	hypothetical prote
58	59.3	302	1 A38097	urate oxidase (EC
59	59.3	309	2 E72784	probable dihydroor
60	59.3	319	2 B71332	conserved hypotet
61	59.3	387	2 B90436	hypothetical prote
62	59.3	475	2 E81810	hypothetical prote
63	59.3	519	2 S54014	hypothetical prote
64	59.3	599	2 A57701	sterol esterase (E
65	59.3	600	2 E87665	arginyl-tRNA synth
66	59.3	612	2 A34967	sterol esterase (E
67	59.3	703	1 A27883	propionyl-CoA carb
68	59.3	943	2 C82559	isoleucyl-tRNA syn
69	59.3	1857	2 T50513	hypothetical prote
70	58.5	388	2 AE2412	aspartate aminotra
71	57.6	130	2 S41123	ribosomal protein
72	57.6	130	2 C75601	probable ribosomal
73	57.6	137	2 A70615	DNA-binding protei
74	57.6	154	2 T34818	hypothetical prote
75	57.6	182	2 T38587	probable semialdeh
76	57.6	226	2 T30695	probable uracil DN
77	57.6	229	2 T51227	histone H1A - Afri
78	57.6	249	2 T04300	probable proteasom
79	57.6	252	2 A49232	outer membrane pro
80	57.6	286	2 H88175	protein T24H7.1 (i
81	57.6	289	1 S39991	Cytochrome-c oxida
82	57.6	289	2 F95344	FixP1 Di-heme cyto
83	57.6	342	2 T34348	hypothetical prote
84	57.6	386	2 T47234	O-succinylthiomoser
85	57.6	387	2 A82036	fatty oxidation co
86	57.6	398	2 C95378	hypothetical prote
87	57.6	481	2 B70179	conserved hypotet
88	57.6	537	2 A55929	zinc finger protei
89	57.6	549	2 AH3224	two component sens
90	57.6	587	2 E84808	hypothetical prote
91	57.6	589	2 F87626	sensor histidine k
92	57.6	627	2 A99607	hypothetical prote
93	57.6	644	2 S39356	transcription fact
94	57.6	668	1 Q0BEW1	UL52 protein - hum
95	57.6	708	2 S70834	transcription init
96	57.6	724	2 T47149	hypothetical prote
97	57.6	741	2 B49555	enhancer of split
98	57.6	771	2 S35681	ESG protein - mous
99	57.6	772	2 D86695	transducin-like en
100	57.6	779	2 T20654	hypothetical prote

## ALIGNMENTS

## RESULT 1

EAHU  
 elastin precursor, long splice form - human  
 N/Alternate names: tropoelastin  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Jun-1990 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C/Accession: A32707; A33705; A30524; A53891  
 R/Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987  
 A/Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA  
 A/Reference number: A32707; MUID: 87289668; PMID: 3039501  
 A/Accession: A32707  
 A/Molecule type: mRNA  
 A/Residues: 1-500, 507-792 <IND>  
 A/Cross-references: UNIPROT:P15502; UNIPROT:Q9UNK5; GB:M16983; GB:J02948  
 R/Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.  
 J. Biol. Chem. 264, 8887-8891, 1989  
 A/Title: Characterization of the complete human elastin gene. Delineation of unusual features  
 A/Reference number: A33705; MUID: 89255358; PMID: 2722804  
 A/Accession: A33705  
 A/Molecule type: DNA  
 A/Residues: 1-27 <BAS>  
 A/Cross-references: GB:J04821; NID:G182052; PIDN:AAA52379.1; PID:G553276  
 R/Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.  
 J. Invest. Dermatol. 91, 458-464, 1988  
 A/Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA library  
 A/Reference number: A30524; MUID: 89009960; PMID: 3171221  
 A/Accession: A30524  
 A/Molecule type: mRNA  
 A/Residues: 1-453, 463-617, 651-792 <PAZ>  
 A/Cross-references: EMBL:M36860; NID:G182061; PIDN:AAA52382.1; PID:G182062  
 A/Note: this sequence represents a composite of several splice forms  
 R/Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; Uitto  
 Lab. Invest. 58, 270-277, 1988  
 A/Title: Isolation and characterization of human elastin cDNAs, and age-associated variations  
 A/Reference number: A53891; MUID: 88156138; PMID: 2831431  
 A/Accession: A53891  
 A/Molecule type: mRNA  
 A/Residues: 164-453, 483-500, 507-617, 651-792 <FA2>  
 A/Cross-references: GB:M24782; NID:G182063; PIDN:AAA53190.1; PID:G182064  
 C/Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix  
 C/Genetics: none  
 A/Gene: GDB:ELN  
 A/Map position: 7q11.23-7q11.23  
 A/Cross-references: GDB:119107; OMIM:130160  
 C/Superfamily: elastin  
 C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
 F;1-26/Domain: signal sequence #status predicted <SIG>  
 F;27-792/Product: elastin #status predicted <MAT>  
 F;782-787/Disulfide bonds: #status predicted

Query Match 100.0%; Score 59; DB 1; Length 792;  
 Best Local Similarity 100.0%; Pred. No. 0.028;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13  
 |||||  
 Db 654 ALAAAKAAYGAA 666

RESULT 2  
 S59623  
 tropoelastin - sheep  
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C/Date: 23-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S59623; A24758  
 R/Nauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; Bo  
 Matrix Biol. 14, 635-641, 1994  
 A/Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.

A/Reference number: S59623

A/Accession: S59623

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-770 &lt;MAJ&gt;

A/Cross-references: UNIPROT:P11547

R/Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smith

Arch. Biochem. Biophys. 241, 684-691, 1985

A/Title: Analysis of the 3' region of the sheep elastin gene.

A/Reference number: A24758; MUID: 85305763; PMID: 3839997

A/Accession: A24758

A/Molecule type: mRNA

A/Residues: 655-669, 671-716, 732-770 &lt;YOO&gt;

A/Superfamily: elastin

C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
 F;760-765/Disulfide bonds: #status predicted

Query Match 91.5%; Score 54; DB 2; Length 770;

Best Local Similarity 92.3%; Pred. No. 0.19;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13

|||||

Db 322 ALAAAKAAYGAA 334

## RESULT 3

EAMS

elastin precursor - mouse

N/Alternate names: tropoelastin

C/Species: Mus musculus (house mouse)

C/Date: 18-Aug-1995 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C/Accession: A55721

R/Wynder, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.

Genomics 23, 125-131, 1994

A/Title: Use of an intron length polymorphism to localize the tropoelastin gene to mouse

A/Reference number: A55721; MUID: 95130069; PMID: 7829060

A/Accession: A55721

A/Molecule type: mRNA

A/Residues: 1-860 &lt;WID&gt;

A/Cross-references: UNIPROT:P54320; GB:U08210; NID:G473273; PIDN:AAA80155.1; PID:G473274

C/Genetics:

A/Map position: 5

C/Superfamily: elastin

C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
 F;1-27/Domain: signal sequence #status predicted <SIG>  
 F;28-860/Product: elastin #status predicted <MAT>

F;850-855/Disulfide bonds: #status predicted

Query Match 89.8%; Score 53; DB 1; Length 860;

Best Local Similarity 92.3%; Pred. No. 0.32;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13

|||||

Db 363 ALAAAKAAYGAA 375

## RESULT 4

EART

elastin precursor - rat

N/Alternate names: tropoelastin

C/Species: Rattus norvegicus (Norway rat)

C/Date: 11-Jan-1991 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C/Accession: A36106; A30878; A36523; S02173; 154172; 168505

R/Pierce, R.A.; Deak, S.B.; Stollie, C.A.; Boyd, C.D.

Biochemistry 29, 9677-9683, 1990

A/Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.

A/Reference number: A36106; MUID: 91104868; PMID: 1702999

A/Accession: A36106

A/Molecule type: mRNA

A/Residues: 1-864 &lt;PIE&gt;

A/Cross-references: UNIPROT:Q99372; GB:M60647; GB:J05292; NID:G207444; PIDN:AAA42269.1;

R;Peak, S.B.; Pierce, R.A.; Beisky, S.A.; Riley, D.J.; Boyd, C.D.  
 J. Biol. Chem. 263, 13504-13507, 1988  
 A;Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.  
 A;Reference number: A30878; MUID:98330868; PMID:2971041  
 A;Accession: A30878  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 781-864 <DEA>  
 A;Cross-references: GB:J04035; NID:G207442; PIDN:AAA42268.1; PID:G207443  
 R;Franzblau, C.; Pratt, C.A.; Faris, B.; Colaninno, N.M.; Offner, G.D.; Mogayzel Jr., P.  
 J. Biol. Chem. 264, 15115-15119, 1989  
 A;Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells.  
 A;Reference number: A36523; MUID:99359327; PMID:2768256  
 A;Accession: A36523  
 A;Molecule type: protein  
 A;Residues: 22-31 <FRA>  
 R;Rich, C.B.; Foster, J.A.  
 Arch. Biochem. Biophys. 268, 551-558, 1989  
 A;Title: Characterization of rat heart tropoelastin.  
 A;Reference number: S02173; MUID:89117149; PMID:2913947  
 A;Accession: S02173  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 'ip', 369-545, 548-764, 770-864 <RIC>  
 A;Experimental source: heart  
 R;Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.  
 Genomics 12, 651-658, 1992  
 A;Title: Elements of the rat tropoelastin gene associated with alternative splicing.  
 A;Reference number: I54172; MUID:92241859; PMID:1572637  
 A;Accession: I54172  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 264-533 <RES>  
 A;Cross-references: GB:M86372; NID:G207455; PIDN:AAA42271.1; PID:G554527  
 A;Accession: I68505  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 558-864 <RE2>  
 A;Cross-references: GB:M86376; NID:G207459; PIDN:AAA42272.1; PID:G207462  
 C;Genetics:  
 A;Introns: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1;  
 A;Note: the list of introns may be incomplete  
 C;Superfamily: elastin  
 C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-864/Product: elastin #status predicted <MAT>  
 F;854-859/Disulfide bonds: #status predicted  
 Query Match 89.8%; Score 53; DB 1; Length 864;  
 Best Local Similarity 92.3%; Pred. No. 0.32; Mismatches 1; Indels 0; Gaps 0;  
 Matches 12; Conservative 0;  
 QY 1 ALAAAKAAKYGAA 13  
 DB 349 AKAAAKAAKYGAA 361  
 RESULT 5  
 EABO  
 N;Alternate names: tropoelastin  
 N;Contains: elastin precursor, splice form b; elastin precursor, splice form c  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 08-Jun-1989 #sequence revision 26-Jul-1996 #text change 09-Jul-2004  
 C;Accession: A31865; A26728; C26728; A22343; I45886  
 R;Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams,  
 Biochemistry 28, 2365-2370, 1989  
 A;Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing.  
 A;Reference number: A31865; MUID:89274159; PMID:2543440  
 A;Accession: A31865  
 A;Molecule type: DNA  
 A;Residues: 1-27 <YEH>  
 A;Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:G340504; PIDN:AAA3077

R;Raju, K.; Anwar, R.A.  
 J. Biol. Chem. 262, 5755-5762, 1987  
 A;Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of cDNA clones.  
 A;Reference number: A92640; MUID:87194772; PMID:3032943  
 A;Accession: A26728  
 A;Molecule type: mRNA  
 A;Residues: 1, 'RS', 4-11, 'E', 13-636, 'V', 638-747 <RAJ>  
 A;Cross-references: GB:J02717; NID:G163019; PIDN:AAA30503.1; PID:G163020  
 A;Accession: B26728  
 A;Molecule type: mRNA  
 A;Residues: 1, 'RS', 4-11, 'E', 13-225, 240-636, 'V', 638-747 <EA2>  
 A;Cross-references: GB:K03505; NID:G163025; PIDN:AAA30505.1; PID:G163026  
 A;Accession: C26728  
 A;Molecule type: mRNA  
 A;Residues: 1, 'RS', 4-11, 'E', 13-225, 260-636, 'V', 638-747 <RA3>  
 A;Cross-references: GB:K03506; NID:G163027; PIDN:AAA30506.1; PID:G163028  
 R;Cicila, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbloom, J.  
 Biochemistry 24, 3075-3080, 1985  
 A;Title: Structure of the 3' portion of the bovine elastin gene.  
 A;Reference number: A22343; MUID:85280426; PMID:2992576  
 A;Accession: A22343  
 A;Molecule type: DNA  
 A;Residues: 613-747 <CIC>  
 A;Cross-references: GB:M20415  
 R;Rosenbloom, J.  
 Lab. Invest. 51, 605-623, 1984  
 A;Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.  
 A;Reference number: I45885; MUID:95059254; PMID:6150137  
 A;Accession: I45886  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 678-683, 685-747 <ROS>  
 A;Cross-references: GB:M31898; NID:G163015; PIDN:AAA96417.1; PID:G163018  
 R;Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.  
 Biochem. Biophys. Res. Commun. 186, 549-555, 1992  
 A;Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an intramolecular disulfide bond.  
 A;Reference number: A58621; MUID:92337651; PMID:1632791  
 C;Contents: annotation, disulfide bonds  
 C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix elastin.  
 C;Genetics:  
 A;Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3  
 A;Note: the list of introns is incomplete  
 C;Superfamily: elastin  
 C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine  
 F;1-747/Product: elastin precursor, splice form a #status predicted <EPA>  
 F;1-225,260-747/Product: elastin precursor, splice form c #status predicted <EPC>  
 F;1-225,240-747/Product: elastin precursor, splice form b #status predicted <EPB>  
 F;1-26/Domain: signal sequence #status predicted <SIG>  
 F;27-747/Product: elastin #status predicted <MAT>  
 F;105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,681,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000  
 Query Match 84.7%; Score 50; DB 1; Length 747;  
 Best Local Similarity 84.6%; Pred. No. 0.9;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ALAAAKAAKYGAA 13  
 DB 319 AAAAKAAKFGAA 331  
 RESULT 6  
 A26601  
 N;Alternate names: tropoelastin  
 C;Species: Gallus gallus (chicken)  
 C;Date: 05-Oct-1988 #sequence revision 26-Jul-1996 #text change 09-Jul-2004  
 C;Accession: A26601; A30795; A27264  
 R;Bressan, G.M.; Argos, P.; Stanley, K.K.  
 Biochemistry 26, 1497-1503, 1987  
 A;Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning.  
 A;Reference number: A26601; MUID:87242320; PMID:3593675

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, K.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AH3110

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-375 <KUR>

A:Cross-references: UNIPROT:Q8U7E1; GB:AE008689; PIDN:AA45302.1; PID:g17742991; GSPDB:C58

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu4508

A:Map position: linear chromosome

Query Match 67.8%; Score 40; DB 2; Length 375;

Best Local Similarity 75.0%; Pred. No. 24;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAAKAAKYGAA 13  
||| |||||:|

DB 47 LAAKAAKFGFA 58  
||| |||||:|

RESULT 9

D98176

hypothetical protein AGR\_L 720 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004

C:Accession: D98176

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughry, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: D98176

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-375 <KUR>

A:Cross-references: UNIPROT:Q8U7E1; GB:AE007870; PIDN:AAK89934.1; PID:g15158710; GSPDB:G

C:Genetics:

A:Gene: AGR\_L 720

A:Map position: linear chromosome

Query Match 67.8%; Score 40; DB 2; Length 375;

Best Local Similarity 75.0%; Pred. No. 24;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAAKAAKYGAA 13  
||| |||||:|

DB 47 LAAKAAKFGFA 58  
||| |||||:|

RESULT 10

A97052

probable lytic murein transglycosylase (N-term. LysM motif repeat domain) CAC1232 [import

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C:Accession: A97052

J:R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC824

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: A97052

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <KUR>

A:Cross-references: UNIPROT:Q97JF1; GB:AE001437; PIDN:AAK79204.1; PID:g15024157; GSPDB:G

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:



A;Gene: CAC1232  
Query Match 66.1%; Score 39; DB 2; Length 253;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ALAAAKAAYGGA 12  
:|||||:  
Db 207 SLGAAGAAYGGS 218  
:  
RESULT 11  
D42653  
dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Acholeplasma laidlawii (fragment)  
N;Alternate names: 36k protein  
C;Species: Acholeplasma laidlawii  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: D42653  
R;Wallbrant, P.; Tegman, V.; Jonsson, B.H.; Wieslander, A.  
J. Bacteriol. 174, 1388-1396, 1992  
A;Title: Identification and analysis of the genes coding for the putative pyruvate dehydrogenase complex in A. laidlawii  
A;Reference number: A42653; MUID:92138635; PMID:1735725  
A;Accession: D42653  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-336 <WAL>  
A;Cross-references: UNIPROT:P35484; GB:M81753; NID:G141807; PIDN:AAA21910.1; PID:G141811  
A;Note: sequence extracted from NCBI backbone (NCBI:79683, NCBI:P:79691)  
C;Keywords: FAD; flavoprotein; lipoamide; NAD; oxidoreductase; redox-active disulfide  
Query Match 66.1%; Score 39; DB 2; Length 336;  
Best Local Similarity 72.7%; Pred. No. 33;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 LAATAAKAAYGGA 12  
:|||||:  
Db 18 VAAIKAAQYGA 28  
:  
RESULT 12  
F87448  
succinylglutamic semialdehyde dehydrogenase [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C;Accession: F87448  
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of Caulobacter crescentus.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: F87448  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-485 <STO>  
A;Cross-references: UNIPROT:Q9ATW2; GB:AE005673; NID:G13423006; PIDN:AAK23586.1; GSPDB:C  
C;Genetics:  
A;Gene: CCL607  
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology  
Query Match 66.1%; Score 39; DB 2; Length 485;  
Best Local Similarity 72.7%; Pred. No. 45;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ALAAAKAAYGGA 11  
:|||||:  
Db 391 ALAAANATRYG 401  
:  
RESULT 13  
A34337  
propionyl-CoA carboxylase (EC 6.4.1.3) alpha chain precursor - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 11-Jan-2002  
C;Accession: A34337; A30871  
R;Browner, M.F.; Taroni, F.; Sztul, E.; Rosenberg, L.E.  
J. Biol. Chem. 264, 12680-12685, 1989  
A;Title: Sequence analysis, biogenesis, and mitochondrial import of the alpha-subunit of  
A;Reference number: A34337; MUID:89308706; PMID:2745462  
A;Accession: A34337  
A;Molecule type: mRNA  
A;Residues: MPYERFCATRCWNSG', 1-704 <BR1>  
A;Cross-references: GB:M22631  
R;Browner, M.F.; Taroni, F.; Sztul, E.; Rosenberg, L.E.  
submitted to GenBank, February 1989  
A;Reference number: A30871  
A;Accession: A30871  
A;Molecule type: mRNA  
A;Residues: MPYERFCATRCWNSG', 1-298, 'WP', 301-704 <BR2>  
A;Cross-references: GB:M22631; NID:G206049; PIDN:AAA88512.1; PID:G206050  
R;Browner, M.F.; Taroni, F.; Sztul, E.; Rosenberg, L.E.  
J. Biol. Chem. 266, 4660, 1991  
A;Reference number: A43040  
A;Contents: annotation; correction  
A;Note: the first 17 residues in the original paper were derived from bacterial DNA as ar  
C;Genetics:  
A;Gene: PCCA  
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl  
C;Keywords: biotin binding; heterododecamer; ligase; mitochondrial matrix; mitochondrion  
F;1-27/Domain: transit peptide (mitochondrion) (fragment) #status predicted <TNP>  
F;28-704/Product: propionyl-CoA carboxylase alpha chain #status predicted <MAT>  
F;41-492/Domain: biotin carboxylase homology <BCH>  
F;631-704/Domain: lipoyl/biotin-binding homology <LPB>  
F;670/Binding site: biotin (Lys) (covalent) #status predicted  
Query Match 64.4%; Score 38; DB 2; Length 704;  
Best Local Similarity 61.5%; Pred. No. 93;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ALAAAKAAYGGA 13  
:|||||:  
Db 296 AVALAKAVKYSSA 308  
:  
RESULT 14  
F71000  
hypothetical protein PH1302 - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
C;Accession: F71000  
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic ar  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: F71000  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-860 <KAW>  
A;Cross-references: UNIPROT:O59003; GB:AP000006; NID:G3236133; PIDN:BAA30406.1; PID:dl031  
A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH1302  
Query Match 64.4%; Score 38; DB 2; Length 860;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 LAATAAKAAYGGA 13  
:|||||:  
Db 826 LTAAGVKYGEA 837  
:  
RESULT 15  
S33422

hypothetical protein 183 - Streptomyces ambofaciens  
 C:Species: Streptomyces ambofaciens  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: S33422  
 R:Hagege, J.M.; Boccard, F.; Smokvina, T.; Pernodet, J.L.; Friedmann, A.; Guerineau, M.  
 submitted to the EMBL Data Library, January 1993  
 A:Description: Identification of a gene encoding the replication initiator protein of th  
 A:Reference number: S33422  
 A:Accession: S33422  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-183 <HAG>  
 A:Cross-references: UNIPROT:P36892; EMBL:Z19594; NID:g298046; PIDN:CAA79646.1; PID:g5753  
 C:Genetics:  
 A:Start codon: GTG

Query Match 62.7%; Score 37; DB 2; Length 183;  
 Best Local Similarity 75.0%; Pred. No. 41;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 12  
 ||||| |||||  
 Db 160 ALAAADAANYAA 171

RESULT 16  
 F95262  
 hypothetical protein Sma0013 [imported] - Sinorhizobium meliloti (strain 1021) magapla  
 C:Species: Sinorhizobium meliloti  
 C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
 C:Accession: F95262  
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
 A>Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot  
 A:Reference number: A95262; MUID:21396509; FMID:11481432  
 A:Accession: F95262  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-244 <KUR>

A:Cross-references: UNIPROT:Q931D6; GB:AE006469; PIDN:AAK64664.1; PID:g14523061; GSPDB:G  
 A:Experimental source: strain 1021, megaplasmid pSymA  
 R:Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
 hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
 A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: Sma0013  
 A:Genome: plasmid

Query Match 62.7%; Score 37; DB 2; Length 244;  
 Best Local Similarity 61.5%; Pred. No. 54;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 13  
 ||||| |||||  
 Db 4 ALARAQAGYGSA 16

RESULT 17  
 E36914  
 molybdate-binding protein homolog ModA - Rhodobacter capsulatus  
 C:Species: Rhodobacter capsulatus  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
 C:Accession: E36914  
 R:Wang, G.; Angermuller, S.; Klipp, W.  
 J. Bacteriol. 175, 3031-3042, 1993  
 A>Title: Characterization of Rhodobacter capsulatus genes encoding a molybdenum transpor

A:Reference number: A36914; MUID:93259949; PMID:8491722

A:Accession: E36914  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-252 <WAN>  
 A:Cross-references: UNIPROT:Q08383; GB:L06254; NID:g310272; PIDN:AAA71911.1; PID:g310276  
 A>Note: sequence extracted from NCBI backbone (NCBIN:131915, NCBI:P131920)  
 C:Superfamily: Molybdate-binding periplasmic protein ModA

Query Match 62.7%; Score 37; DB 1; Length 252;  
 Best Local Similarity 61.5%; Pred. No. 55;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 13  
 ||||| |||||  
 Db 135 AJADPKSAPYGAA 147

RESULT 18  
 G75468  
 hypothetical protein - Deinococcus radiodurans (strain RL)  
 C:Species: Deinococcus radiodurans  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: G75468  
 R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 ; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma.  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999

A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RL.  
 A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: G75468  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-285 <WHI>  
 A:Cross-references: UNIPROT:Q9RM12; GB:AE001939; GB:AE000513; NID:g6458563; PIDN:AAF1043  
 A:Experimental source: strain RL  
 C:Genetics:  
 A:Gene: DR0857  
 A:Map position: 1

Query Match 62.7%; Score 37; DB 2; Length 285;  
 Best Local Similarity 61.5%; Pred. No. 62;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 13  
 ||||| |||||  
 Db 12 ALGACAAARHGAA 24

RESULT 19  
 S09208  
 chorion protein s36 - Mediterranean fruit fly  
 C:Species: Ceratitis capitata (Mediterranean fruit fly)  
 C>Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 09-Jul-2004  
 C:Accession: S09208  
 R:Konsolaki, M.; Komitopoulou, K.; Tolia, P.P.; King, D.L.; Swimmer, C.; Kafatos, F.C.  
 Nucleic Acids Res. 18, 1731-1737, 1990  
 A>Title: The chorion genes of the medfly, Ceratitis capitata, I: structural and regulato  
 A:Reference number: S09208; MUID:90245561; PMID:1692403  
 A:Accession: S09208  
 A:Molecule type: DNA  
 A:Residues: 1-320 <KON>  
 A:Cross-references: UNIPROT:P17110; EMBL:X51342; NID:g5973; PIDN:CAA35723.1; PID:g295730  
 C:Genetics:  
 A:Introns: 14/3

Query Match 62.7%; Score 37; DB 2; Length 320;  
 Best Local Similarity 72.7%; Pred. No. 68;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAAAKAAKYGA 13  
 :||| |||||  
 Db 273 SAAPAAASYGAA 283

```
RESULT 20
E71201
probable glucose-fructose oxidoreductase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: E71201
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71201
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-335 <KAW>
A;Cross-references: UNIPROT:O59537; GB:AF000007; NID:g3236134; PIDN:BAA31004.1; PID:g325
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1882

Query Match 62.7%; Score 37; DB 2; Length 335;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 12
||| :|||
Db 40 ALAKVEAKKYGA 51
||| :|||

RESULT 21
D91240
probable amino acid amidohydrolase [imported] - Escherichia coli (strain O157:H7, subst
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D91240
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91240
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <HAY>
A;Cross-references: UNIPROT:O8X726; GB:BA000007; PIDN:BA838315.1; PID:g13364368; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECS4892
C;Superfamily: hippurate hydrolase

Query Match 62.7%; Score 37; DB 2; Length 388;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 12
||| :|||
Db 273 ALAQQAASFGA 284
||| :|||

RESULT 22
A86088
probable hippuricase Z5522 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A86088
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
```

```
A;Accession: A86088
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <STO>
A;Cross-references: UNIPROT:Q8X726; GB:AE005174; NID:g12518888; PIDN:AAG59165.1; GSPDB:GN
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z5522
C;Superfamily: hippurate hydrolase

Query Match 62.7%; Score 37; DB 2; Length 388;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 12
||| :|||
Db 273 ALAQQAASFGA 284
||| :|||

RESULT 23
G70693
probable dinF protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70693
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70693
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-439 <COL>
A;Cross-references: UNIPROT:P71616; GB:Z81331; GB:AL123456; NID:g3261650; PIDN:CAB03650.1
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: dinF
C;Superfamily: conserved hypothetical protein H11612

Query Match 62.7%; Score 37; DB 2; Length 439;
Best Local Similarity 72.7%; Pred. No. 91;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAARKAAKYGAA 13
||| :|||
Db 252 AAARPAARPGAA 262
||| :|||

RESULT 24
C83998
acetyl-CoA carboxylase biotin carboxylase subunit accC [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83998
R;Takami, H.; Nakabone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83998
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-452 <STO>
A;Cross-references: UNIPROT:Q9K963; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA8065
A;Experimental source: strain C-125
C;Genetics:
A;Gene: accC
C;Superfamily: biotin carboxylase; biotin carboxylase homology

Query Match 62.7%; Score 37; DB 2; Length 452;
Best Local Similarity 61.5%; Pred. No. 93;
```

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
|:|||||

Db 259 AVAAAKAVNSGA 271  
|:|||||

RESULT 25  
E95367  
probable methyltransferase - chemotaxis [imported] - Sinorhizobium meliloti (strain 1021)  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: E95367  
R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: E95367  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-453 <RUR>  
A:Cross-references: UNIPROT:Q92YM8; GB:AE006469; PIDN:AAK65503.1; PID:gl4523976; GSPDB:G  
A:Experimental source: strain 1021, megaplasmid pSymA  
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
Peia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: SMal552  
A:Genome: plasmid

Query Match 62.7%; Score 37; DB 2; Length 453;  
Best Local Similarity 72.7%; Pred. No. 93;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYG 11  
|:|||||

Db 142 ALAAAKTGDYG 152  
|:|||||

RESULT 26  
T36807  
probable aldehyde dehydrogenase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T36807  
R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, July 1999  
A:Reference number: Z21614  
A:Accession: T36807  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-462 <OLI>  
A:Cross-references: UNIPROT:Q9S246; EMBL:AL096811; PIDN:CAB46804.1; GSPDB:GN00070; SCOR  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCORDB:SCI30A.27C  
C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 62.7%; Score 37; DB 2; Length 462;  
Best Local Similarity 72.7%; Pred. No. 95;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYG 11  
|:|||||

Db 297 SLAAEAAAKYG 307  
|:|||||

## RESULT 27

QJWNPB

photosystem II chlorophyll a-binding protein psbB precursor - Prochlorothrix hollandica  
N;Alternate names: photosystem II CP-47 protein  
C:Species: Prochlorothrix hollandica

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: S17739

R; Greer, K.L.; Golden, S.S.  
Plant Mol. Biol. 17, 915-917, 1991

A:Title: Nucleotide sequence of psbB from Prochlorothrix hollandica.  
A:Reference number: S17739; MUID:92003701; PMID:1840692

A:Accession: S17739

A:Molecule type: DNA

A:Residues: 1-514 <GRE>

A:Cross-references: UNIPROT:P27200; EMBL:X59614; NID:g45537; PIDN:CAA42177.1; PID:g45538

A:Note: the authors translated the codon CCC for residue 134 as O  
C:Genetics:

A:Gene: psbB

C:Superfamily: photosystem II chlorophyll a-binding protein psbB  
C:Keywords: chlorophyll; photosynthesis; photosystem II; transmembrane protein  
F;19-40/Domain: transmembrane #status predicted <TM1>  
F;104-120/Domain: transmembrane #status predicted <TM2>  
F;146-162/Domain: transmembrane #status predicted <TM3>  
F;211-227/Domain: transmembrane #status predicted <TM4>  
F;245-261/Domain: transmembrane #status predicted <TM5>  
F;459-475/Domain: transmembrane #status predicted <TM6>

Query Match

62.7%; Score 37; DB 1; Length 514;

Best Local Similarity 69.2%; Pred. No. 1e+02;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13

|:|||||

Db 245 ALASATAAVFGAA 257

## RESULT 28

T39993

N2,N2-dimethylguanosine tRNA methyltransferase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: T39993

R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Whithead, S.; Chillingworth, T.; Church,

submitted to the EMBL Data Library, July 1998

A:Reference number: Z21897

A:Accession: T39993

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-524 <LYN>

A:Cross-references: EMBL:AL031158; PIDN:CAA20101.1; GSPDB:GN00067; SPDB:SPBC25D12.05

A:Experimental source: strain 972h-; cosmid c25D12

C:Genetics:

A:Gene: SPDB:SPBC25D12.05

A:Map position: 2

Query Match

62.7%; Score 37; DB 2; Length 524;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAKAAKYGAA 13

|:|||||

Db 245 AASAAKYGRA 254

## RESULT 29

T46565

tRNA (guanine-N2-)-methyltransferase (EC 2.1.1.32) [imported] - fission yeast (Schizosac

C:Species: Schizosaccharomyces pombe

C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004

C:Accession: T46565

R; Niederberger, C.

submitted to the EMBL Data Library, February 1998

A;Description: Cloning and characterization of the putative tRNA (guanine-N2-)-methyltra

A;Reference number: Z23073

A;Accession: I46585

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-548 <NIE>

A;Cross-references: UNIPROT:Q9P804; EMBL:AJ224000; PIDN:CAA11801.1

C;Genetics:

A;Gene: trml

C;Keywords: methyltransferase; S-adenosylmethionine

Query Match 62.7%; Score 37; DB 2; Length 548;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AAKAAKYGAA 13  
|||  
Db 269 AASAAKYGRA 278

# RESULT 30

A86926

probable membrane protein [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C;Accession: A86926

R;Cole, S.T.; Bigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Title: Massive gene decay in the leprosy bacillus

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: A86926

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-902 <STO>

A;Cross-references: GB:AL450380; NID:gl3092515; PIDN:CAC29645.1; GSPDB:GN00147

C;Genetics:

A;Gene: mmpL7

Query Match 62.7%; Score 37; DB 2; Length 902;  
Best Local Similarity 63.6%; Pred. No. 1.7e+02;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LAATAAKAYGA 12  
:|:|:|:|:|:  
Db 699 IAAGKAMKYS 709

Search completed: November 19, 2004, 16:38:49  
Job time : 4.58472 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 2.62838 Seconds

(without alignments)  
2845.805 Million cell updates/sec

Title: US-09-743-818A-13

Perfect score: 59

Sequence: 1 ALAAAKAAYGAA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	258	2	Q9UMF5
2	59	100.0	472	2	Q8N2G0
3	59	100.0	570	2	Q6ZWG6
4	59	100.0	570	2	BAC85506
5	59	100.0	658	2	Q6P0L4
6	59	100.0	658	2	AAH65566
7	59	100.0	687	2	Q14235
8	59	100.0	687	2	Q72316
9	59	100.0	711	2	Q7Z3F5
10	59	100.0	730	1	ELUS_HUMAN
11	59	100.0	757	2	Q14234
12	59	100.0	757	2	Q75MU5
13	59	100.0	757	2	AA07435
14	54	91.5	559	2	Q6ZUM2
15	54	91.5	559	2	BAC86188
16	54	91.5	602	2	Q15337
17	54	91.5	635	2	Q15336
18	54	91.5	643	2	Q8NB14
19	53	89.8	810	2	Q9ESZ9
20	53	89.8	860	1	ELUS_MOUSE
21	53	89.8	860	2	Q8C9L8
22	53	89.8	864	1	ELUS_RAT
23	50	84.7	650	2	Q28099
24	50	84.7	666	2	Q28096
25	50	84.7	679	2	Q28097
26	50	84.7	707	2	Q28098
27	50	84.7	747	1	ELUS_BOVIN
28	50	84.7	750	1	ELUS_CHICK
29	47	79.7	69	2	Q28101
30	47	79.7	100	1	ELUS_SHEEP
31	43	72.9	382	2	Q8YNN3

32	41	69.5	277	2	Q7X738	Oryza sativa
33	41	69.5	277	2	CAE03060	Oryza sativa
34	40	67.8	375	2	Q7CV49	Agrobacterium
35	40	67.8	375	2	Q8U7E1	Agrobacterium
36	40	67.8	393	2	Q75803	Agrobacterium
37	40	67.8	393	2	AAS52343	Agrobacterium
38	40	67.8	421	2	Q8U7Y9	Agrobacterium
39	40	67.8	649	2	Q6CXW7	Agrobacterium
40	39	66.1	133	2	Q9RL42	Agrobacterium
41	39	66.1	253	2	Q970P1	Agrobacterium
42	39	66.1	329	1	Q9NHE0	Agrobacterium
43	39	66.1	336	1	DLDH_ACHLA	Agrobacterium
44	39	66.1	448	2	Q9A7W2	Agrobacterium
45	38	64.4	145	1	AROQ_CORGL	Agrobacterium
46	38	64.4	145	1	AAQ64007	Agrobacterium
47	38	64.4	149	2	Q9S6G5	Agrobacterium
48	38	64.4	155	2	Q9LMB3	Agrobacterium
49	38	64.4	177	2	Q9SNF2	Agrobacterium
50	38	64.4	275	1	HXDC_HUMAN	Agrobacterium
51	38	64.4	294	2	Q6J7W5	Agrobacterium
52	38	64.4	294	2	AAT36814	Agrobacterium
53	38	64.4	474	2	Q7VFP30	Agrobacterium
54	38	64.4	531	2	Q8L476	Agrobacterium
55	38	64.4	724	2	Q8OVU5	Agrobacterium
56	38	64.4	724	2	Q91ZA3	Agrobacterium
57	38	64.4	724	2	Q922N3	Agrobacterium
58	38	64.4	860	2	Q59003	Agrobacterium
59	38	64.4	1401	2	Q7S799	Agrobacterium
60	38	64.4	1472	2	Q9L214	Agrobacterium
61	37	62.7	76	2	Q28100	Agrobacterium
62	37	62.7	76	2	AAAG6416	Agrobacterium
63	37	62.7	152	2	Q7XT75	Agrobacterium
64	37	62.7	152	2	Q9FSP3	Agrobacterium
65	37	62.7	183	1	YREP_STRAM	Agrobacterium
66	37	62.7	183	2	Q9ADC3	Agrobacterium
67	37	62.7	183	2	CAA06454	Agrobacterium
68	37	62.7	244	2	Q931D6	Agrobacterium
69	37	62.7	252	1	MODA_RHOCA	Agrobacterium
70	37	62.7	277	2	Q73XE9	Agrobacterium
71	37	62.7	277	2	AAS04557	Agrobacterium
72	37	62.7	285	2	Q9RM12	Agrobacterium
73	37	62.7	289	2	Q6NJK4	Agrobacterium
74	37	62.7	289	2	CAE48901	Agrobacterium
75	37	62.7	320	1	CH36_CERCA	Agrobacterium
76	37	62.7	332	2	Q939Q8	Agrobacterium
77	37	62.7	335	2	Q95537	Agrobacterium
78	37	62.7	336	2	Q6N298	Agrobacterium
79	37	62.7	336	2	CAE29593	Agrobacterium
80	37	62.7	349	2	Q8LGO6	Agrobacterium
81	37	62.7	353	2	Q6H521	Agrobacterium
82	37	62.7	371	2	Q812E7	Agrobacterium
83	37	62.7	385	2	Q82DF6	Agrobacterium
84	37	62.7	388	2	Q7A966	Agrobacterium
85	37	62.7	388	2	Q8FB92	Agrobacterium
86	37	62.7	388	2	Q8X726	Agrobacterium
87	37	62.7	436	2	Q7D6H3	Agrobacterium
88	37	62.7	439	2	P71616	Agrobacterium
89	37	62.7	439	2	Q7TXR0	Agrobacterium
90	37	62.7	452	2	Q9K963	Agrobacterium
91	37	62.7	453	2	Q92YN8	Agrobacterium
92	37	62.7	462	2	Q9S246	Agrobacterium
93	37	62.7	487	2	Q6W253	Agrobacterium
94	37	62.7	487	2	AAQ87165	Agrobacterium
95	37	62.7	501	2	Q8HS72	Agrobacterium
96	37	62.7	501	2	Q6NBI9	Agrobacterium
97	37	62.7	501	2	CAE26283	Agrobacterium
98	37	62.7	514	1	PSBB_PROHO	Agrobacterium
99	37	62.7	531	2	Q826R5	Agrobacterium
100	37	62.7	548	1	TRM1_SCHPO	Agrobacterium

ALIGNMENTS

```
RESULT 1
Q9UMF5
ID Q9UMF5 PRELIMINARY; PRT; 258 AA.
AC Q9UMF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96411691; PubMed=8812460;
RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
RA Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,
RA Koop B.F., Tsui L.-C.;
RT "Comparative genomic sequence analysis of the Williams syndrome region
RT (LIMK1-RFC2) of human chromosome 7q11.23."
RL Mamm. Genome 11:890-898(2000).
DR EMBL: U63721; AAC13884.1; -.
DR InterPro; IPR001451; Hexapep.transf.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 258 AA; 21990 MW; C39BF7298D0E05D2 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
Db 120 ALAAAKAAKYGAA 132

RESULT 2
Q8N2G0
ID Q8N2G0 PRELIMINARY; PRT; 472 AA.
AC Q8N2G0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PSEC0191.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK073494; BAC11651.1; -.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 472
```

```
SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
Db 360 ALAAAKAAKYGAA 372

RESULT 3
Q6ZMJ6
ID Q6ZMJ6 PRELIMINARY; PRT; 570 AA.
AC Q6ZMJ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16246.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Osuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK122731; BAC85506.1; -.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;

Query Match 100.0%; Score 59; DB 2; Length 570;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
Db 450 ALAAAKAAKYGAA 462

RESULT 4
BAC85506
ID BAC85506 PRELIMINARY; PRT; 570 AA.
AC BAC85506;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin
DE gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Osuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
```



RT "NEDO human cDNA sequencing project."  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK122731; BAC85506.1; -  
 SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;

Query Match 100.0%; Score 59; DB 2; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 0.17;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13  
 |||||  
 Db 450 ALAAKAAKYGAA 462

RESULT 5  
 Q6P0L4 PRELIMINARY; PRT; 658 AA.  
 AC Q6P0L4  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ELN protein.  
 GN Name=ELN;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC065566; AAH65566.1; -  
 DR InterPro; IPR001451; Hexapep transf.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOELASTIN.  
 DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.  
 SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 658;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13  
 |||||  
 Db 538 ALAAKAAKYGAA 550

RESULT 6  
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 AC Q6P0L4  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ELN protein.  
 GN Name=ELN;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC065566; AAH65566.1; -  
 DR InterPro; IPR001451; Hexapep transf.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOELASTIN.  
 DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.  
 SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 658;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13  
 |||||  
 Db 538 ALAAKAAKYGAA 550

RESULT 6

AAH65566  
 ID AAH65566 PRELIMINARY; PRT; 658 AA.  
 AC AAH65566;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ELN protein.  
 GN ELN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
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 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC065566; AAH65566.1; -  
 DR EMBL; BC065566; AAH65566.1; -  
 SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 658;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13  
 |||||  
 Db 538 ALAAKAAKYGAA 550

RESULT 7  
 Q14235 PRELIMINARY; PRT; 687 AA.  
 AC Q14235;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Elastin.  
 GN Name=ELN;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87289668; PubMed=3039501;  
 RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,  
 RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;  
 RT "Alternative splicing of human elastin mRNA indicated by sequence  
 analysis of cloned genomic and complementary DNA.";

Qy 1 ALAAKAAKYGAA 13  
 |||||  
 Db 538 ALAAKAAKYGAA 550

RESULT 6



RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,  
RA Rosenbloom J., Uitto J.;  
RT "Isolation and characterization of human elastin cDNAs, and age-  
RT associated variation in elastin gene expression in cultured skin  
RT fibroblasts.";  
RL Lab. Invest. 58:270-277 (1988).  
RN [4]  
RP SEQUENCE OF 603-730 FROM N.A.  
RC TISSUE=Hippocampus, and Placenta;  
RX MEDLINE=96291399; PubMed=8689686;  
RA Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,  
RA Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,  
RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,  
RA Keating W.T.;  
RT "LIM-kinase hemizygosity implicated in impaired visuospatial  
RT constructive cognition.";  
RL Cell 86:59-63 (1996).  
RN [5]  
RP INVOLVEMENT IN CUTIS LAXA.  
RX MEDLINE=99091639; PubMed=9873040;  
RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;  
RT "Cutis laxa arising from frameshift mutations in exon 30 of the  
RT elastin gene (ELN).";  
RL J. Biol. Chem. 274:981-986 (1999).  
RN [6]  
RP INVOLVEMENT IN SVAS.  
RX PubMed=10942104;  
RA Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonenfant J.-P.,  
RA Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;  
RT "Isolated supravalvular aortic stenosis: functional haploinsufficiency  
RT of the elastin gene as a result of nonsense-mediated decay.";  
RL Hum. Genet. 106:577-588 (2000).  
CC -!- FUNCTION: Major structural protein of tissues such as aorta and  
CC nuchal ligament, which must expand rapidly and recover completely.  
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together  
CC into an extensible 3D network.  
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Comment=Additional isoforms seem to exist;  
CC Name=1;  
CC IsoId=P15502-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P15502-2; Sequence=VSP\_004243;  
CC -!- PM: The crosslinks are made of deaminated Lys.  
CC -!- DISEASE: Defects in ELN are a cause of autosomal dominant cutis  
CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder  
CC characterized by loose, hyperextensible skin with decreased  
CC resilience and elasticity leading to a premature aged appearance.  
CC The skin changes are often accompanied by extracutaneous  
CC manifestations, including pulmonary emphysema, bladder  
CC diverticula, pulmonary artery stenosis and pyloric stenosis.  
CC -!- DISEASE: Haploinsufficiency of ELN may be the cause of certain  
CC cardiovascular and musculo-skeletal abnormalities observed in  
CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare  
CC developmental disorder and a contiguous gene deletion syndrome  
CC involving genes from chromosome band 7q11.23.  
CC -!- DISEASE: Defects in ELN are the cause of supravalvular aortic  
CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of  
CC the ascending aorta which can occur sporadically, as an autosomal  
CC dominant condition, or as one component of Williams-Beuren  
CC syndrome.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M17282; AAC98394.1; JOINED.  
DR EMBL; M16983; AAC98394.1; JOINED.

DR EMBL; M17265; AAC98394.1; JOINED.  
DR EMBL; M17266; AAC98394.1; JOINED.  
DR EMBL; M17267; AAC98394.1; JOINED.  
DR EMBL; M17268; AAC98394.1; JOINED.  
DR EMBL; M17270; AAC98394.1; JOINED.  
DR EMBL; M17271; AAC98394.1; JOINED.  
DR EMBL; M17272; AAC98394.1; JOINED.  
DR EMBL; M17273; AAC98394.1; JOINED.  
DR EMBL; M17275; AAC98394.1; JOINED.  
DR EMBL; M17276; AAC98394.1; JOINED.  
DR EMBL; M17277; AAC98394.1; JOINED.  
DR EMBL; M17278; AAC98394.1; JOINED.  
DR EMBL; M17279; AAC98394.1; JOINED.  
DR EMBL; M17280; AAC98394.1; JOINED.  
DR EMBL; M17281; AAC98394.1; JOINED.  
DR EMBL; M36860; AAA52382.1; -.  
DR EMBL; M24782; AAB17544.1; -.  
DR EMBL; U62292; AAB17544.1; -.  
DR EMBL; X15603; CAA33627.1; -.  
DR PIR; A32707; EAHU.  
DR HSP; P50099; IZFU.  
DR Genew; HGNC:3327; ELN.  
DR MIM; 130160; -.  
DR MIM; 123700; -.  
DR MIM; 194050; -.  
DR MIM; 185500; -.  
DR GO; GO:0005578; C:extracellular matrix; TAS.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.  
DR GO; GO:0008283; P:cell proliferation; TAS.  
DR GO; GO:0008015; P:circulation; TAS.  
DR GO; GO:0007887; P:organogenesis; TAS.  
DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.  
DR InterPro; IPR003979; tropoelastin.  
DR PRINTS; PR01500; TROPOELASTIN.  
DR KW Alternative splicing; Connective tissue; Repeat; Signal;  
DR Structural protein; Williams-Beuren syndrome.  
FT SIGNAL 1 26  
FT CHAIN 27 730 Elastin.  
FT DISULFID 720 725 By similarity.  
FT VARSPPLIC 472 477 Missing (in isoform 2).  
FT FTID=VSP\_004243.  
SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;  
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Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 ALAAAKAAKYGAA 13  
Db 592 ALAAAKAAKYGAA 604  
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ID Q14234  
AC Q14234;  
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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Elastin.  
GN Name=ELN;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87289668; PubMed=3039501;  
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,  
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;  
RT "Alternative splicing of human elastin mRNA indicated by sequence  
RT analysis of cloned genomic and complementary DNA.";

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Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=87274906; PubMed=3038460;
Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
"Structure of the 3' region of the human elastin gene: great abundance
of Alu repetitive sequences and few coding sequences.";
Connect. Tissue Res. 16:197-211(1987).
EMBL; M17282; AAC98395.1; -.
EMBL; M16983; AAC98395.1; JOINED.
EMBL; M17265; AAC98395.1; JOINED.
EMBL; M17266; AAC98395.1; JOINED.
EMBL; M17267; AAC98395.1; JOINED.
EMBL; M17268; AAC98395.1; JOINED.
EMBL; M17270; AAC98395.1; JOINED.
EMBL; M17271; AAC98395.1; JOINED.
EMBL; M17272; AAC98395.1; JOINED.
EMBL; M17273; AAC98395.1; JOINED.
EMBL; M17274; AAC98395.1; JOINED.
EMBL; M17275; AAC98395.1; JOINED.
EMBL; M17276; AAC98395.1; JOINED.
EMBL; M17277; AAC98395.1; JOINED.
EMBL; M17278; AAC98395.1; JOINED.
EMBL; M17279; AAC98395.1; JOINED.
EMBL; M17280; AAC98395.1; JOINED.
EMBL; M17281; AAC98395.1; JOINED.
GO; GO:0005578; C:extracellular matrix; NAS.
GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
InterPro; IPR001451; Hexapep.transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROP0ELASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN 1.
SEQUENCE 757 AA; 66136 MW; 2387F5B8AF85CA8_CRC64;

Query Match 100.0%; Score 59; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAATAAKAAYGAA 13
Db |||||
619 ALAATAAKAAYGAA 631

RESULT 12
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ID Q75MU5 PRELIMINARY; PRT; 757 AA.
AC Q75MU5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Hypothetical protein ELN.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=22737999; PubMed=12853948;
RX Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Fell G.A., Delhaunt K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Stromatt J.P.,
Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
Wend M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
Hicklenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
Gillitt W., Zhou Y., James R., Phelps K., Iadamoto S., Bub K.,
Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
Waterston R.H., Wilson R.K.;
"The DNA sequence of human chromosome 7.";
Nature 424:157-164(2003).
RN [2]
SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005056; AAS07435.1; -.
InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738_CRC64;

Query Match 100.0%; Score 59; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAATAAKAAYGAA 13
Db |||||
619 ALAATAAKAAYGAA 631

RESULT 13
AAS07435
ID AAS07435 PRELIMINARY; PRT; 757 AA.
AC AAS07435;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE Hypothetical protein ELN.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=22737999; PubMed=12853948;
RX Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Fell G.A., Delhaunt K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Stromatt J.P.,
Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
Wend M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
Hicklenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
Gillitt W., Zhou Y., James R., Phelps K., Iadamoto S., Bub K.,
Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
Waterston R.H., Wilson R.K.;
"The DNA sequence of human chromosome 7.";

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RL Nature 424:157-164 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Du H., Rohlfing T., Strong C.;
RT "The sequence of Homo sapiens BAC clone CTE-51J22.";
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP Waterston R.H.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RP Waterston R.;
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: AC005056; AAS07435.1; -.
RW Hypothetical protein.
SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
Db 619 ALAAAKAAYGAA 631

RESULT 14
Q6ZUN2 PRELIMINARY; PRT; 559 AA.
AC Q6ZUN2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43523.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: AK125511; BAC6188.1; -.
RW Hypothetical protein.
SQ SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 559;
Best Local Similarity 92.3%; Pred. No. 1.1;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
Db 302 ALAAAKAAYGAA 314

RESULT 15
BAC6188 PRELIMINARY; PRT; 559 AA.
AC BAC6188;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: AK125511; BAC6188.1; -.
RW Hypothetical protein.
SQ SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 559;
Best Local Similarity 92.3%; Pred. No. 1.1;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
Db 302 ALAAAKAAYGAA 314

RESULT 16
O15337 PRELIMINARY; PRT; 602 AA.
ID O15337;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP MEDLINE=97358574; PubMed=9215670;
RX Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RA "Elastin point mutations cause an obstructive vascular disease,
RT supravalvular aortic stenosis.";
RL Hum. Mol. Genet. 6:1021-1028 (1997).
DR EMBL: U93037; AAB65620.1; -.
DR EMBL: U93034; AAB65620.1; JOINED.
DR EMBL: U93035; AAB65620.1; JOINED.
DR EMBL: U93036; AAB65620.1; JOINED.
DR GO: GO:0005578; C:extracellular matrix; IEA.
DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro: IPR001451; Hexapep transf.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS: PR01500; TROPOELASTIN
DR PROSITE: PS00101; HEXAPEP_TRANSFEROSES; UNKNOWN_1.
FT NON TER 1
FT NON TER 602
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 602;
Best Local Similarity 92.3%; Pred. No. 1.2;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
Db 302 ALAAAKAAYGAA 314

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```
Db 279 AAAAAKAAKYGAA 291
Query Match 91.5%; Score 54; DB 2; Length 643;
Best Local Similarity 92.3%; Pred. No. 1.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 17
O15336 PRELIMINARY; PRT; 635 AA.
ID O15336;
AC O15336;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358574; PubMed=9215670;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RT "Elastin point mutations cause an obstructive vascular disease,
RT supraaortic aortic stenosis.";
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL; U93037; AAB65621.1; -.
DR EMBL; U93034; AAB65621.1; JOINED.
DR EMBL; U93035; AAB65621.1; JOINED.
DR EMBL; U93036; AAB65621.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 635
SQ SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 635;
Best Local Similarity 92.3%; Pred. No. 1.2;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAKAAKYGAA 13
| | | | | | | | | |
Db 279 AAAAAKAAKYGAA 291

RESULT 18
Q8NB14 PRELIMINARY; PRT; 643 AA.
ID Q8NB14;
AC Q8NB14;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein P5EC0254.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075554; BAC11696.1; -.
DR HSP; F50099; IZFU.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 643 AA; 55629 MW; FDFC042617E72A69 CRC64;

Db 279 AAAAAKAAKYGAA 291
Query Match 91.5%; Score 54; DB 2; Length 643;
Best Local Similarity 92.3%; Pred. No. 1.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAKAAKYGAA 13
| | | | | | | | | |
Db 313 AAAAAKAAKYGAA 325

RESULT 20
ELS_MOUSE STANDARD; PRT; 860 AA.
ID ELS_MOUSE
AC P54320;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=Elm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c; TISSUE=Lung;
RX MEDLINE=95130069; PubMed=7829060;
RA Wyder K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
RT "Use of an intron polymorphism to localize the tropoelastin gene to
RT mouse chromosome 5 in a region of linkage conservation with human
RT chromosome 7.";
RL Genomics 23:125-131(1994).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- PTM: The crosslinks are made of deaminated Lys.
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DR EMBL; U08210; AAA80155.1; --  
 DR PIR; A55721; EAMS.  
 DR MGD; MGI:95317; Eln.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOLASTIN.  
 KW Connective tissue; Repeat; Signal; Structural protein.  
 FT SIGNAL 1 27 Potential.  
 FT CHAIN 28 860 Elastin.  
 FT DISULFID 850 855 By similarity.  
 SQ SEQUENCE 860 AA; 71955 MW; 0C0BB5AAE1EDD7F1 CRC64;

Query Match 89.8%; Score 53; DB 1; Length 860;  
 Best Local Similarity 92.3%; Pred. No. 2.4;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAAKAAKYGAA 13

Db 363 AKAAAKAAKYGAA 375

RESULT 21

Q8C9L8 PRELIMINARY; PRT; 860 AA.  
 AC Q8C9L8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched  
 DE library, clone:A630042119 product:elastin, full insert sequence  
 DE (Elastin).  
 DE Name=Eln;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=21085660; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA The FANTOM Consortium,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes";

RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Izawa Y., Izawa M., Ohara E., Watanabe M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume M.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
 RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK041860; BAC31084.1; -.  
 DR EMBL; BC051649; AAHS1649.1; -.  
 DR MGD; MGI:95317; Eln.  
 DR GO; GO:0007519; P:myogenesis; IMP.  
 DR GO; GO:0030833; P:regulation of actin filament polymerization; IMP.  
 DR GO; GO:0043149; P:stress fiber formation; IMP.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOLASTIN.  
 SQ SEQUENCE 860 AA; 71938 MW; 7C340F2FFDC92E5 CRC64;

Query Match 89.8%; Score 53; DB 2; Length 860;  
 Best Local Similarity 92.3%; Pred. No. 2.4;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;





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RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30499.1; -.
DR EMBL; M11422; AAA30499.1; JOINED.
DR EMBL; M19366; AAA30499.1; JOINED.
DR EMBL; M19368; AAA30499.1; JOINED.
DR EMBL; M19369; AAA30499.1; JOINED.
DR EMBL; M19370; AAA30499.1; JOINED.
DR EMBL; M19371; AAA30499.1; JOINED.
DR EMBL; M22771; AAA30499.1; JOINED.
DR EMBL; M22772; AAA30499.1; JOINED.
DR EMBL; M22773; AAA30499.1; JOINED.
DR EMBL; M22774; AAA30499.1; JOINED.
DR EMBL; M22775; AAA30499.1; JOINED.
DR EMBL; M22988; AAA30499.1; JOINED.
DR EMBL; M23010; AAA30499.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 650 AA; 55373 MW; CD21ABB3E9076AD7 CRC64;

Query Match 84.7%; Score 50; DB 2; Length 650;
Best Local Similarity 84.6%; Pred.No. 5.9;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13
Db 230 ALAAKAAKYGAA 242
|||||:|||||

RESULT 24
Q28096 PRELIMINARY; PRT; 666 AA.
AC Q28096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Elastin-cBE13; NCBI gi: 163005 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30501.1; -.
DR EMBL; M11422; AAA30500.1; JOINED.
DR EMBL; M19366; AAA30500.1; JOINED.
DR EMBL; M19367; AAA30500.1; JOINED.
DR EMBL; M19368; AAA30500.1; JOINED.
DR EMBL; M19369; AAA30500.1; JOINED.
DR EMBL; M19370; AAA30500.1; JOINED.
DR EMBL; M19371; AAA30500.1; JOINED.
DR EMBL; M22771; AAA30500.1; JOINED.
DR EMBL; M22772; AAA30500.1; JOINED.
DR EMBL; M22773; AAA30500.1; JOINED.
DR EMBL; M22774; AAA30500.1; JOINED.
DR EMBL; M22988; AAA30500.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 679 AA; 57652 MW; EB3C019E3BD7618D CRC64;

Query Match 84.7%; Score 50; DB 2; Length 679;

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DR EMBL; M19370; AAA30501.1; JOINED.
DR EMBL; M19371; AAA30501.1; JOINED.
DR EMBL; M22771; AAA30501.1; JOINED.
DR EMBL; M22772; AAA30501.1; JOINED.
DR EMBL; M22773; AAA30501.1; JOINED.
DR EMBL; M22774; AAA30501.1; JOINED.
DR EMBL; M22775; AAA30501.1; JOINED.
DR EMBL; M22988; AAA30501.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro: IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 666 AA; 56435 MW; BCB5E62632BE1B71 CRC64;

Query Match 84.7%; Score 50; DB 2; Length 666;
Best Local Similarity 84.6%; Pred.No. 6.1;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13
Db 230 ALAAKAAKYGAA 242
|||||:|||||

RESULT 25
Q28097 PRELIMINARY; PRT; 679 AA.
AC Q28097;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Elastin-cBE12; NCBI gi: 163004 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
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RX MEDLINE=8028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30500.1; -.
DR EMBL; M11422; AAA30500.1; JOINED.
DR EMBL; M19366; AAA30500.1; JOINED.
DR EMBL; M19367; AAA30500.1; JOINED.
DR EMBL; M19368; AAA30500.1; JOINED.
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DR EMBL; M22773; AAA30500.1; JOINED.
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DR EMBL; M22988; AAA30500.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
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DR InterPro: IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 679 AA; 57652 MW; EB3C019E3BD7618D CRC64;

Query Match 84.7%; Score 50; DB 2; Length 679;

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Best Local Similarity 84.6%; Pred. No. 6.2;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 264 ALAAAKAAYGAA 276

RESULT 26
Q28098 PRELIMINARY; PRT; 707 AA.
AC Q28098;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Elastin; NCBI gi: 163002 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30498.1; -.
DR EMBL; M11422; AAA30498.1; JOINED.
DR EMBL; M19366; AAA30498.1; JOINED.
DR EMBL; M19367; AAA30498.1; JOINED.
DR EMBL; M19368; AAA30498.1; JOINED.
DR EMBL; M19369; AAA30498.1; JOINED.
DR EMBL; M19370; AAA30498.1; JOINED.
DR EMBL; M19371; AAA30498.1; JOINED.
DR EMBL; M22771; AAA30498.1; JOINED.
DR EMBL; M22772; AAA30498.1; JOINED.
DR EMBL; M22773; AAA30498.1; JOINED.
DR EMBL; M22774; AAA30498.1; JOINED.
DR EMBL; M22775; AAA30498.1; JOINED.
DR EMBL; M22988; AAA30498.1; JOINED.
DR EMBL; M23010; AAA30498.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 707 AA; 60346 MW; FDFD59BAB34CE33 CRC64;

Query Match 84.7%; Score 50; DB 2; Length 707;
Best Local Similarity 84.6%; Pred. No. 6.4;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 264 ALAAAKAAYGAA 276

RESULT 27
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ID ELN BOVIN STANDARD; PRT; 747 AA.
AC P04985; P04986; P04987; Q29421;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
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OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RX MEDLINE=87194772; PubMed=3032943;
RA Raju K., Anwar R.A.;
RT "Primary structures of bovine elastin a, b, and c deduced from the
RT sequences of cDNA clones.";
RL J. Biol. Chem. 262:5755-5762(1987).
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RX TISSUE=Nuchal ligament;
RT MEDLINE=89274159; PubMed=2543440;
RA Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
RA Rosenbloom J.;
RT "Structure of the bovine elastin gene and SI nuclease analysis of
RT alternative splicing of elastin mRNA in the bovine nuchal ligament.";
RL Biochemistry 28:2365-2370(1989).
RN [3]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=91234332; PubMed=2031719;
RA Manohar A., Shi W., Anwar R.A.;
RT "Partial characterization of bovine elastin gene; comparison with the
RT gene for human elastin.";
RL Biochem. Cell Biol. 69:185-192(1991).
RN [4]
RP DISULFIDE BOND.
RX MEDLINE=92337851; PubMed=1632791;
RA Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
RT "The cysteine residues in the carboxy terminal domain of tropoelastin
RT form an intrachain disulfide bond that stabilizes a loop structure and
RT positively charged pocket.";
RL Biochem. Biophys. Res. Commun. 186:549-555(1992).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=A;
CC IsoId=P04985-1; Sequence=Displayed;
CC Name=2; Synonyms=B;
CC IsoId=P04985-2; Sequence=VSP_004239;
CC Name=3; Synonyms=C;
CC IsoId=P04985-3; Sequence=VSP_004240;
CC -!- PTM: The crosslinks are made of deaminated Lys.
CC -----
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CC -----
DR EMBL; J02717; AAA30503.1; -
DR EMBL; K03505; AAA30505.1; -
DR EMBL; K03506; AAA30506.1; -
DR EMBL; J02855; AAA30776.1; -
DR EMBL; M58652; AAA03519.2; -
DR PIR; A31865; EABO.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN
KW Alternative splicing; Connective tissue; Repeat; Signal;
KW Structural protein.
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FT CONFLICT 12 12 E -> G (in Ref. 2 and 3).
FT SEQUENCE 747 AA; 64229 MW; 633C03E411643D83 CRC64;

Query Match 84.7%; Score 50; DB 1; Length 747;
Best Local Similarity 84.6%; Pred. NO. 6.7;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 AAAAAKAAKVGAA 13
Db 319 AAAAAKAAKFGAA 331

RESULT 28
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DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin) (Fragment).
GN Name=ELN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCB1_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87242320; PubMed=3593675;
RA Bressan G.M., Argos P., Stanley K.K.;
RT "Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning.";
RN Biochemistry 26:1497-1503 (1987).
RN [2]
RP SEQUENCE OF 85-750 FROM N.A. (ISOFORM 2).
RX MEDLINE=88309083; PubMed=2841924;
RA Baule V.J., Foster J.A.;
RT "Multiple chick tropoelastin mRNAs.";
RN Biochem. Biophys. Res. Commun. 154:1054-1060 (1988).
RN [3]
RP SEQUENCE OF 457-750 FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=87297534; PubMed=3502711;

```

Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;  
 "Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcription of the elastin gene in developing chick embryo."; Arch. Biochem. Biophys. 256:455-461 (1987).  
 -!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.  
 -!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.  
 -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.  
 -!- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=2;  
 Comment=Additional isoforms seem to exist;  
 Name=1;  
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 Name=2; Synonyms=Embryonic;  
 IsoId=P07916-2; Sequence=VSP\_004241, VSP\_004242;  
 -!- PTM: The crosslinks are made of deaminated Lys.  
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 EMBL; M21880; AAA49082.1; -;  
 EMBL; M15889; AAA49108.1; -;  
 PIR; A26601; A26601.  
 InterPro; IPR008160; Collagen.  
 InterPro; IPR003979; tropoelastin.  
 Pfam; PF01391; Collagen; 1.  
 PRINTS; PR01500; TROPOLASTIN.  
 KW Alternative splicing; Connective tissue; Repeat; Signal;  
 Structural protein.  
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 FT SIGNAL <1 24 Elastin.  
 FT CHAIN 25 750 8 X tandem repeats.  
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 FT REPEAT 83 127 2.  
 FT REPEAT 219 262 3.  
 FT REPEAT 263 318 4.  
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 FT REPEAT 394 482 6.  
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 FT REPEAT 555 619 8.  
 FT REPEAT 620 686 By similarity.  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:37:11 ; Search time 84.1092 Seconds  
(without alignments)  
2168.321 Million cell updates/sec

Title: US-09-743-818A-71

Perfect score: 2680

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Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	2667	99.5	730	10	US-09-961-403-8
4	2431	90.7	692	15	US-10-210-172-40
5	2306.5	86.1	663	15	US-10-108-260A-2477
6	2129.5	79.5	617	14	US-10-104-047-2915
7	911.5	34.0	745	9	US-09-837-969A-38
8	911.5	34.0	745	9	US-09-841-321A-38
9	890	33.2	988	8	US-08-806-029-28
10	872	32.5	832	8	US-08-806-029-27
11	870.5	32.5	965	16	US-10-800-179-31
12	870	32.5	936	8	US-08-806-029-26
13	864	32.2	1056	8	US-08-806-029-29
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225					Sequence 40, Appl
226					Sequence 2477, Ap
227					Sequence 2915, Ap
228					Sequence 38, Appl
229					Sequence 38, Appl
230					Sequence 28, Appl
231					Sequence 27, Appl
232					Sequence 31, Appl
233					Sequence 26, Appl
234					Sequence 29, Appl
235					Sequence 1, Appl
236					Sequence 38, Appl
237					Sequence 8, Appl
238					Sequence 40, Appl
239					Sequence 2477, Ap
240					Sequence 2915, Ap
241					Sequence 38, Appl
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246					Sequence 26, Appl
247					Sequence 29, Appl
248					Sequence 1, Appl
249					Sequence 38, Appl
250					Sequence 8, Appl
251					Sequence 40, Appl
252					Sequence 2477, Ap

87 550 20.5 1128 17 US-10-479-638-49 Sequence 49, Appl  
88 539.5 20.1 714 9 US-09-861-597-10 Sequence 10, Appl  
89 531.5 19.8 1130 16 US-10-720-025-61 Sequence 61, Appl  
90 527 19.7 2304 17 US-10-479-638-53 Sequence 53, Appl  
91 524 19.6 720 14 US-10-342-331-4 Sequence 4, Appl  
92 522.5 19.5 830 16 US-10-720-025-58 Sequence 58, Appl  
93 519 19.4 1136 8 US-08-806-029-9 Sequence 9, Appl  
94 519 19.4 1177 14 US-10-096-986-64 Sequence 64, Appl  
95 516.5 19.3 821 16 US-10-720-025-51 Sequence 51, Appl  
96 516 19.3 520 17 US-10-479-638-21 Sequence 21, Appl  
97 514.5 19.2 504 14 US-10-342-331-3 Sequence 3, Appl  
98 509 19.0 1759 14 US-10-369-493-7032 Sequence 7032, Ap  
99 501.5 18.7 525 17 US-10-479-638-16 Sequence 16, Appl  
100 501 18.7 780 15 US-10-441-965-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-09-964-662-1  
; Sequence 1, Application US/09964662  
; Publication No. US20030166846A1  
; GENERAL INFORMATION:  
; APPLICANT: PROTEIN SPECIALTIES LTD.  
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP  
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND  
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS  
; FILE REFERENCE: 041082/0112  
; CURRENT APPLICATION NUMBER: US/09/964,662  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: 09/340,736  
; PRIOR FILING DATE: 1999-06-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-662-1

Query Match 99.6%; Score 2670; DB 10; Length 731;  
Best Local Similarity 99.6%; Pred. No. 6.1e-139;  
Matches 513; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGVPGAIPGCVPGGVYPGAGLGGALGGGKPLKVPVGGLAGAGLGAGLGAFFAVT 60  
DB 1 GGVPGAIPGCVPGGVYPGAGLGGALGGGKPLKVPVGGLAGAGLGAGLGAFFAVT 60  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGGGVPGVGLGVSAGAVVPPQAGVKPKVPGVGL 120  
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DB 181 PKAPKLPGGYGLPYTTGKLPYGYGGGVAGAGKAGYPTGTGVGQAAAAAAXKAAKF 240  
QY 241 GAGAAGVLPVGGGAGVPGVPGALPGIIGGIAGVGTAAAAAAXKAAKAAAGLVPGG 300  
DB 241 GAGAAGVLPVGGGAGVPGVPGALPGIIGGIAGVGTAAAAAAXKAAKAAAGLVPGG 300  
QY 301 PGFPGVWVPGAGVPGVPGVPGAGIPVVPAGITPGAAVPGVSPPEAAAAKAAKAYGAR 360  
DB 301 PGFPGVWVPGAGVPGVPGVPGAGIPVVPAGITPGAAVPGVSPPEAAAAKAAKAYGAR 360  
QY 361 PGVGVGGIPTYGVGAGGFPFGVGGIPGVAGVPGVGGVPGVGGVPGVGGISPEAQAAA 420  
DB 361 PGVGVGGIPTYGVGAGGFPFGVGGIPGVAGVPGVGGVPGVGGVPGVGGISPEAQAAA 420

QY 421 AKAAKYGVGTAAAAAAXKAAQFGLVPGVGVGVPAGVGVGVPAGVGLAPGVGVPAG 480  
DB 421 AKAAKYGVGTAAAAAAXKAAQFGLVPGVGVGVPAGVGVGVPAGVGLAPGVGVPAG 480  
QY 481 VGVPGVGVGVPAGVGVGVPAGVGVGVPAGVGVGVPAGVGVGVPAGVGVGVPAG 515  
DB 481 VGVPGVGVGVPAGVGVGVPAGVGVGVPAGVGVGVPAGVGVGVPAGVGVGVPAG 515

RESULT 2

US-10-210-172-38  
; Sequence 38, Application US/10210172  
; Publication No. US20040043928A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Pena, Carol  
; APPLICANT: Rieger, Daniel  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Li, Li  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Casman, Stacie  
; APPLICANT: Voss, Edward  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gorman, Linda  
; APPLICANT: Leite, Mario  
; APPLICANT: Vernet, Corine  
; APPLICANT: Anderson, David  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zhong, Mei  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Hjal, Tord  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: MacDougall, John  
; APPLICANT: Stone, David  
; APPLICANT: Alsobrook II, John  
; APPLICANT: Lepley, Denise et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-416 A  
; CURRENT APPLICATION NUMBER: US/10/210,172  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/309,501  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/323,994  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/373,814  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/310,291  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 60/310,951  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/310,544  
; PRIOR FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 60/311,292  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/311,979  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 60/313,201  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/312,892  
; PRIOR FILING DATE: 2001-08-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 327  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 38  
; LENGTH: 711

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 19, 2004, 16:06:25 ; Search time 23.1638 Seconds  
(without alignments)  
2139.188 Million cell updates/sec

Title: US-09-743-818A-71  
Perfect score: 2680  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_79:\*\*

1: pir1:\*\*  
2: pir2:\*\*  
3: pir3:\*\*  
4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2642.5	98.6	792	1 EAHU	elastin precursor,
2	1964.5	73.3	770	2 S59623	tropoelastin - she
3	1842.5	68.8	747	1 EABO	elastin precursor,
4	1728.5	64.5	860	1 EAMS	elastin precursor
5	1675.5	62.5	864	1 EART	elastin precursor
6	1432.5	53.5	784	2 A26601	elastin precursor
7	509	19.0	1758	2 T29350	hypothetical prote
8	509	19.0	1759	2 T29351	collagen alpha 2(I
9	494.5	18.5	1763	2 S16366	collagen alpha 2(I
10	489.5	18.3	627	2 A44112	spidiroin 2, dragli
11	488.5	18.2	718	2 A36068	major ampullate fi
12	484.5	18.1	1901	2 F70806	hypothetical glyci
13	478	17.8	1669	1 CGHU4B	collagen alpha 1(I
14	466	17.4	1489	2 D70807	hypothetical glyci
15	456.5	17.0	1669	1 CGMS4B	hypothetical glyci
16	456	17.0	1691	1 S22917	collagen alpha 1(I
17	453.5	16.9	749	2 A70812	hypothetical glyci
18	450	16.8	1329	2 E70917	hypothetical glyci
19	446	16.6	767	2 E70895	hypothetical glyci
20	445.5	16.6	1049	1 CGB07S	collagen alpha 1(I
21	445.5	16.6	2639	2 T31328	collagen alpha 1(I
22	444	16.6	1466	1 CGHU7L	fibroin - Chinese
23	443.5	16.5	1464	2 S59856	collagen alpha 1(I
24	439	16.4	1464	1 CGHU1S	collagen alpha 1(I
25	437.5	16.3	882	2 E70812	hypothetical glyci
26	436.5	16.3	1042	1 CGCHLS	collagen alpha 1(I
27	436	16.3	741	2 G70917	hypothetical glyci
28	434.5	16.2	783	2 E70824	hypothetical glyci
29	434	16.2	1306	2 A70934	hypothetical glyci

30	432	16.1	1373	1 A43291	collagen alpha 2(I
31	430	16.0	754	2 A55267	collagen alpha 5(I
32	429	16.0	812	2 S31521	collagen COLP1 - f
33	428	16.0	778	2 F70963	hypothetical glyci
34	427	15.9	1366	1 CGHU2S	collagen alpha 2(I
35	425.5	15.9	744	1 A34246	collagen alpha 1(V
36	425.5	15.9	744	1 S23298	collagen alpha 1(V
37	425	15.9	1418	2 T45467	collagen alpha 1(I
38	424.5	15.8	779	1 CGB01S	collagen alpha 1(I
39	423.5	15.8	1453	2 S21626	collagen alpha 1(I
40	423	15.8	671	1 CGRT1S	collagen alpha 1(I
41	423	15.8	1492	2 A40333	collagen alpha 1(I
42	422.5	15.8	618	2 A70989	hypothetical glyci
43	421.5	15.7	603	2 A70770	hypothetical glyci
44	421.5	15.7	1712	1 CGHU2B	collagen alpha 2(I
45	420	15.7	801	2 F70824	hypothetical glyci
46	420	15.7	914	2 H70987	hypothetical glyci
47	420	15.7	1660	2 A70869	hypothetical glyci
48	419.5	15.7	1487	1 CGHU6C	collagen alpha 1(I
49	415	15.5	1486	1 B40333	collagen alpha 1(I
50	414	15.4	584	2 G70804	hypothetical glyci
51	412	15.4	744	2 S15435	collagen alpha 1(V
52	412	15.4	1419	2 A41182	collagen alpha 1(I
53	412	15.4	1487	2 B41182	collagen alpha 1(I
54	411	15.3	1381	2 E70806	hypothetical glyci
55	410.5	15.3	2944	2 A54849	collagen alpha 1(V
56	410	15.3	384	1 A26099	glycine-rich cell
57	409	15.3	1691	1 CGHU6B	collagen alpha 6(I
58	406.5	15.2	635	2 A57131	collagen alpha 2(V
59	406.5	15.2	964	1 CGCH2S	collagen alpha 2(I
60	405	15.1	743	1 S23779	collagen alpha 1(V
61	405	15.1	1497	2 I49607	procollagen type V
62	403.5	15.1	957	2 D70835	hypothetical glyci
63	403.5	15.1	1707	2 A33526	collagen alpha 2(I
64	403	15.0	853	2 A70896	hypothetical glyci
65	402.5	15.0	1079	2 B70807	hypothetical glyci
66	401.5	15.0	1690	1 CGHU1B	collagen alpha 4(I
67	401	15.0	674	2 S23297	collagen alpha 1(X
68	401	15.0	1496	1 CGHU2V	collagen alpha 2(V
69	400.5	14.9	408	2 S57483	glycin-rich protei
70	400.5	14.9	694	2 F70868	hypothetical glyci
71	399	14.9	1744	2 S40991	collagen alpha 1(I
72	398	14.9	680	1 CGHU1D	collagen alpha 1(X
73	396.5	14.8	907	2 A45560	sporozoite surface
74	395	14.7	641	1 QCB531	nuclear antigen EB
75	394	14.7	837	2 E70835	hypothetical glyci
76	393.5	14.7	1603	2 S23810	collagen alpha 1(X
77	393.5	14.7	1752	2 A45407	collagen alpha 3(I
78	392	14.6	606	2 H70816	hypothetical glyci
79	391.5	14.6	469	2 A24450	collagen alpha 2(V
80	390	14.6	921	2 S42617	collagen alpha 1(I
81	389.5	14.5	886	2 I50694	collagen alpha 1(I
82	388.5	14.5	1027	2 S28774	collagen alpha cha
83	386	14.4	1806	1 CGHU1E	collagen alpha 1(X
84	385.5	14.4	615	2 H70589	hypothetical glyci
85	384.5	14.3	714	2 A70807	hypothetical glyci
86	384.5	14.3	1538	2 H70846	hypothetical glyci
87	384	14.3	1024	2 S18251	collagen alpha 1(X
88	383.5	14.3	731	2 C70974	collagen alpha 2(I
89	382	14.3	677	2 S23296	collagen alpha 2(I
90	382	14.3	923	2 E70820	hypothetical glyci
91	381.5	14.2	673	1 CGB06C	collagen alpha 1(I
92	381.5	14.2	1670	1 CGHU3B	collagen alpha 3(I
93	381	14.2	921	2 S40495	collagen alpha 1(I
94	378	14.1	674	2 S13301	collagen alpha 1(X
95	377.5	14.1	920	2 B34493	collagen alpha 1(I
96	376.5	14.0	1775	2 A31893	collagen alpha 1(I
97	376	14.0	1414	1 S23809	collagen alpha 2(I
98	375.5	14.0	1549	2 I48103	type VII collagen
99	375	14.0	680	2 S31216	collagen alpha 1(X
100	373.5	13.9	1838	1 CGHU1V	collagen alpha 1(V

## ALIGNMENTS

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elastin precursor, long splice form - human
N/Alternate names: tropoelastin
C/Species: Homo sapiens (man)
C/Date: 22-Jun-1990 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: A33707; A33705; A30524; A53891
R/Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987
A/Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA
A/Reference number: A33707; MUID:87289668; PMID:3039501
A/Accession: A33707
A/Molecule type: mRNA
A/Residues: 1-500,507-792 <IND>
A/Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948
R/Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.
J. Biol. Chem. 264, 8887-8891, 1989
A/Title: Characterization of the complete human elastin gene. Delineation of unusual features
A/Reference number: A33705; MUID:89255358; PMID:2722804
A/Accession: A33705
A/Molecule type: DNA
A/Residues: 1-27 <BAS>
A/Cross-references: GB:J04821; NID:g182052; PIDN:AAAS2379.1; PID:g553276
R/Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.
J. Invest. Dermatol. 91, 458-464, 1988
A/Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA
A/Reference number: A30524; MUID:89009960; PMID:3171221
A/Accession: A30524
A/Molecule type: mRNA
A/Residues: 1-453,483-617,651-792 <FAZ>
A/Cross-references: EMBL:M36860; NID:g182061; PIDN:AAAS2382.1; PID:g182062
A/Note: This sequence represents a composite of several splice forms
R/Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U
Lab. Invest. 58, 270-277, 1988
A/Title: Isolation and characterization of human elastin cDNAs, and age-associated variation
A/Reference number: A53891; MUID:88156138; PMID:2831431
A/Accession: A53891
A/Molecule type: mRNA
A/Residues: 164-453,483-500,507-617,651-792 <FA2>
A/Cross-references: GB:M24782; NID:g182063; PIDN:AAAS3190.1; PID:g182064
C/Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
matrix protein.
C/Genetics:
A/Gene: GDB:ELN
A/Cross-references: GDB:I19107; OMIM:130160
A/Map position: 7q11.23-7q11.23
C/Superfamily: elastin
C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:1-26/Domain: signal sequence #status predicted <SIG>
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F:782-787/Disulfide bonds: #status predicted
Query Match 98.6%; Score 2642.5; DB 1; Length 792;
Best Local Similarity 93.6%; Pred. No. 2.1e-118;
Matches 515; Conservative 0; Mismatches 0; Indels 35; Gaps 2;
QY 1 GGVPGAIPGGVPGVFPYPCAGLGGALGGGKPLKVPVGGLAGAGLGGAGLGAFFAVT 60
DB 27 GGVPGAIPGGVPGVFPYPCAGLGGALGGGKPLKVPVGGLAGAGLGAFFAVT 86
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKPKVPGVL 120
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKPKVPGVL 146
QY 121 PGVPGVGLVPGARFPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGPGVPLGY 180
DB 147 PGVPGVGLVPGARFPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGPGVPLGY 206
QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGTGVPQAAAAAKAAKF 240

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DB 207 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGTGVPQAAAAAKAAKF 266
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DB 267 GAGAAAGVLPVGGAGVPGVPGAIPOIGGIAGVGTTPAAAAAATAAATAAAGLVPGG 326
QY 301 PGFGPGVGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVVSPEAAAKAAAKAAYGAR 360
DB 327 PGFGPGVGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVVSPEAAAKAAAKAAYGAR 386
QY 361 PGVGVGGIPTYTGAGAGGPFPGFVGVPVGVAGVSVGVPGVGVGGISPEAQAAAA 420
DB 387 PGVGVGGIPTYTGAGAGGPFPGFVGVPVGVAGVSVGVPGVGVGGISPEAQAAAA 446
QY 421 AKAAKY-----GVGTPAAAAAKAAAKAAQF----- 445
DB 447 AKAAKYAGAGAGVGLGGLVPGQAAVPGVGTGTVGTEAAAAAKAAAKAAQFALLNLA 506
QY 446 GLVPGVGVAPGVGVAPGVGVGLAPGVGVAPGVGVGVAPGVGVGVAAAAAKSA 505
DB 507 GLVPGVGVAPGVGVAPGVGVGLAPGVGVAPGVGVGVGVGVGVAAAAAKSA 566
QY 506 AKVAAKAQLR 515
DB 567 AKVAAKAQLR 576
RESULT 2
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C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S59623; A24758
R/Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; Smit
Matrix Biol. 14, 635-641, 1994
A/Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.
A/Reference number: S59623
A/Accession: S59623
A/Status: Preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-770 <MAU>
A/Cross-references: UNIPROT:P11547
R/Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smit
Arch. Biochem. Biophys. 241, 684-691, 1985
A/Title: Analysis of the 3' region of the sheep elastin gene.
A/Reference number: A24758; MUID:85305763; PMID:3839997
A/Accession: A24758
A/Molecule type: mRNA
A/Residues: 655-669,671-716,732-770 <YOO>
C/Superfamily: elastin
C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:760-765/Disulfide bonds: #status predicted
Query Match 73.3%; Score 1964.5; DB 2; Length 770;
Best Local Similarity 72.2%; Pred. No. 2.3e-86;
Matches 411; Conservative 18; Mismatches 55; Indels 85; Gaps 16;
QY 1 GGVPGAIPGGVPGVFPYPCAGLGGALGGGKPLKVPVGGLAGAGLGA-GLGAFFAV 59
DB 27 GGVPGAIPGGVPGVFPYPCAGLGGALGGGKPLKVPVGGLAGAGLGA-GLGAFFAV 86
QY 60 TTPGAL--VPGGVADAAAAYK--AAKAGA---GLGVPVGGVGLGVSAGAVVPPQGA--- 108
DB 87 APFGGFFGAGGGAAGAAAYKAAKAGAGLGGVGGIGVGGVGLGVSTGAVFQLGAGVGV 146
QY 109 GVKPKVPGVGLPGVVPVGGVLP--GARFPGVGLFPGVPTGAGVKPKAPGVGGAFAGIPGV 166
DB 147 GVKPKVPGVGLPGVVPVGGVLPFGTGARPPGIGVLPVGTGAGVKPKAPGCGGCRFAGIPGV 206
QY 167 GFPGPGVPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGTGVP 226
DB 207 GFPGGQQQVPLGYPIKAPKLPGGYGLPYSTGKLPYGVGPGVAGAGKAGYPTGTGTGVP 266

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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 104.124 Seconds  
(without alignments)  
2845.805 Million cell updates/sec

Title: US-09-743-818A-71

Perfect score: 2680

Sequence: 1 GGVEGAIPGGVPGGVFPGA.....GGVAAAKSAKVAQAQLR 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2680	100.0	757	Q14234	Q14234 homo sapien
2	2676	99.9	757	Q75MU5	Q75mu5 homo sapien
3	2676	99.9	757	AA07435	AA07435 homo sapi
4	2667	99.5	730	ELS_HUMAN	ELS_HUMAN
5	2659.5	99.2	711	Q7Z3F5	Q7Z3F5 homo sapien
6	2630.5	98.2	602	Q15337	Q15337 homo sapien
7	2630.5	98.2	635	Q15336	Q15336 homo sapien
8	2571.5	96.0	687	Q14235	Q14235 homo sapien
9	2500.5	93.3	687	Q7Z316	Q7Z316 homo sapien
10	2411.5	90.0	658	Q6P014	Q6P014 homo sapien
11	2411.5	90.0	658	AAH65566	AAH65566 homo sapi
12	2161.5	80.7	643	Q8NB14	Q8NB14 homo sapien
13	2023.5	75.5	559	Q6ZUN2	Q6ZUN2 homo sapien
14	2023.5	75.5	559	BAC86188	BAC86188 homo sapi
15	1870	69.8	570	Q6ZM76	Q6ZM76 homo sapien
16	1870	69.8	570	BAC85506	BAC85506 homo sapi
17	1842.5	68.8	747	ELS_BOVIN	ELS_BOVIN
18	1808.5	67.5	679	Q28097	Q28097 bos taurus
19	1808.5	67.5	707	Q28098	Q28098 bos taurus
20	1731.5	64.6	860	Q8C918	Q8C918 mus musculus
21	1728.5	64.5	860	ELS_MOUSE	ELS_MOUSE
22	1675.5	62.5	864	ELS_RAT	ELS_RAT
23	1637.5	61.1	810	Q8ES29	Q8ES29 mus musculus
24	1607.5	60.0	650	Q28099	Q28099 bos taurus
25	1606.5	59.9	666	Q28096	Q28096 bos taurus
26	1314	49.0	472	Q8N2G0	Q8N2G0 homo sapien
27	1291.5	48.2	750	ELS_CHICK	ELS_CHICK
28	797.5	29.8	172	Q9BDZ0	Q9BDZ0 gallus gall
29	614	22.9	1953	Q9BIT7	Q9BIT7 macaca mula
30	600.5	22.4	651	Q9BIU9	Q9BIU9 nephila ina
31	600.5	22.4	988	Q17434	Q17434 argiope tri

32	597.5	22.3	1884	2	Q9NHW2	Q9nhw2 nephila ina
33	592	22.1	1071	2	Q7YU48	Q7yu48 drosophila
34	592	22.1	1713	2	Q9VTR6	Q9vtr6 drosophila
35	581.5	21.7	1002	2	Q9BIU8	Q9biu8 argiope tri
36	581.5	21.7	1729	2	Q9U617	Q9u617 drosophila
37	577	21.5	2249	2	Q9NHW4	Q9nhw4 nephila cla
38	562.5	21.0	907	2	Q44359	Q44359 nephila cla
39	560	20.9	5263	1	FB0H_BOMMO	P05790 bombyx mori
40	540.5	20.2	524	2	Q817U1	Q817u1 araneus ven
41	539.5	20.1	563	2	Q6J6N0	Q6j6n0 araneus ven
42	539.5	20.1	563	2	AA036347	AA036347 araneus v
43	536	20.0	871	2	Q44358	Q44358 nephila cla
44	523.5	19.5	626	2	Q9NHW1	Q9nhw1 nephila ina
45	520	19.4	1666	2	Q7PT93	Q7pt93 anopheles g
46	509	19.0	1758	1	CA24_CAEEL	P17140 caenorhabdi
47	508	19.0	897	2	Q6Q294	Q6q294 agelenopsis
48	508	19.0	897	2	AA08436	AA08436 agelenopsis
49	505.5	18.9	1802	2	Q17163	Q17163 bugia mala
50	500	18.7	1715	2	Q8VI20	Q8viz0 mycobacteri
51	498.5	18.6	617	2	Q46172	Q46172 nephila cla
52	495	18.5	691	2	Q9BIU3	Q9biu3 dolomedes t
53	494.5	18.5	1763	1	CA24_ASCSU	P27393 ascaris suu
54	492.5	18.4	1460	2	Q7TWC3	Q7twc3 mycobacteri
55	491	18.3	1468	2	Q9GUB5	Q9gub5 galleria me
56	489.5	18.3	627	1	SPD2_NEPCL	P46804 nephila cla
57	488.5	18.2	747	1	SPD1_NEPCL	P19837 nephila cla
58	488.5	18.2	894	2	Q8MW54	Q8mw54 mytilus gal
59	488	18.2	644	2	Q8WSW4	Q8wsW4 nephila cla
60	484.5	18.1	1901	1	FG54_MYCTU	O53553 mycobacteri
61	483.5	18.0	760	2	Q6PY84	Q6py84 kukulcania
62	483.5	18.0	760	2	AA08433	AA08433 kukulcani
63	478	17.8	1621	2	Q9H4R9	Q9h4r9 homo sapien
64	478	17.8	1669	1	CA14_HUMAN	P02462 homo sapien
65	474.5	17.7	1075	2	Q86X41	Q86x41 homo sapien
66	471.5	17.6	902	2	O16161	O16161 mytilus edu
67	471.5	17.6	1217	2	Q8VIY9	Q8viy9 mycobacteri
68	469.5	17.5	462	2	Q9NHW3	Q9nhw3 nephila cla
69	467	17.4	992	2	Q7TMB8	Q7tmb8 mycobacteri
70	466.5	17.4	1684	2	Q8HYC1	Q8hycl canis famli
71	466.5	17.4	1691	2	Q86622	Q86622 canis famli
72	466.5	17.4	1691	2	AA033458	AA033458 canis fam
73	466	17.4	1489	2	Q6MMW6	Q6mmw6 mycobacteri
74	466	17.4	1489	2	CAE55607	CAE55607 mycobacte
75	461	17.2	738	2	O02402	O02402 pinctada fu
76	459.5	17.1	1449	2	Q6NZ15	Q6nzi15 brachydanio
77	459.5	17.1	1449	2	Q6PEI9	Q6pei9 brachydanio
78	459.5	17.1	1449	2	AAH66384	AAH66384 brachydan
79	459.5	17.1	1449	2	AAH58045	AAH58045 brachydan
80	456.5	17.0	1562	2	Q6GQS7	Q6gqs7 mus musculu
81	456.5	17.0	1669	1	CA14_MOUSE	P02463 mus musculu
82	456	17.0	1685	1	CA54_HUMAN	P29400 homo sapien
83	455.5	17.0	648	2	Q9BIU7	Q9biu7 argiope tri
84	455	17.0	544	2	O46171	O46171 nephila cla
85	455	17.0	563	2	Q9BIT5	Q9bit5 nephila ina
86	455	17.0	1691	2	Q9ESQ2	Q9esq2 mus musculu
87	454.5	17.0	749	2	Q7D974	Q7d974 mycobacteri
88	454.5	17.0	1408	2	Q7U022	Q7u022 mycobacteri
89	454	16.9	922	2	O44367	O44367 mytilus edu
90	453.5	16.9	749	2	Q79FV7	Q79fv7 mycobacteri
91	453.5	16.9	749	2	CAE55328	CAE55328 mycobacte
92	453	16.9	610	2	Q9V5V8	Q9v5v8 drosophila
93	452.5	16.9	774	2	Q7U0P7	Q7u0p7 mycobacteri
94	452	16.9	773	2	Q7U160	Q7u160 mycobacteri
95	450.5	16.8	258	2	Q9UMF5	Q9umf5 homo sapien
96	450	16.8	1329	2	Q79FP2	Q79fp2 mycobacteri
97	450	16.8	1329	2	CAE55390	CAE55390 mycobacte
98	449.5	16.8	2655	2	Q964F4	Q964f4 antheraea y
99	448	16.7	1464	2	Q8BLW4	Q8blw4 mus musculu
100	446	16.6	767	2	Q79FT0	Q79ft0 mycobacteri

ALIGNMENTS

```

RESULT 1
Q14234 PRELIMINARY; PRT; 757 AA.
AC Q14234;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-WAR-2004 (TReMBLrel. 26, Last annotation update)
DE Elastin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87298668; PubMed=3039501;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
DR EMBL; M17282; AAC98395.1; JOINED.
DR EMBL; M16983; AAC98395.1; JOINED.
DR EMBL; M17265; AAC98395.1; JOINED.
DR EMBL; M17266; AAC98395.1; JOINED.
DR EMBL; M17267; AAC98395.1; JOINED.
DR EMBL; M17268; AAC98395.1; JOINED.
DR EMBL; M17270; AAC98395.1; JOINED.
DR EMBL; M17271; AAC98395.1; JOINED.
DR EMBL; M17272; AAC98395.1; JOINED.
DR EMBL; M17273; AAC98395.1; JOINED.
DR EMBL; M17274; AAC98395.1; JOINED.
DR EMBL; M17275; AAC98395.1; JOINED.
DR EMBL; M17276; AAC98395.1; JOINED.
DR EMBL; M17277; AAC98395.1; JOINED.
DR EMBL; M17278; AAC98395.1; JOINED.
DR EMBL; M17279; AAC98395.1; JOINED.
DR EMBL; M17280; AAC98395.1; JOINED.
DR EMBL; M17281; AAC98395.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; NAS.
DR GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; HEXAPEP TRANSFERASES.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ SEQUENCE 757 AA; 66136 MW; 23B7FE58AF85CA8 CRC64;

Query Match 100.0%; Score 2680; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 1.3e-99;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGLPGGVPVGGVFPAGLGGALGGALGGKPLKVPVGGLAGAGLGGAGPAPVT 60
DB 27 GGVPGLPGGVPVGGVFPAGLGGALGGALGGKPLKVPVGGLAGAGLGGAGPAPVT 86

QY 61 FPGALVPGGVADAAAAKAAKAGAGLGGVPGVGGVAGAVVPPQAGVKKPGKVPVGL 120
DB 87 FPGALVPGGVADAAAAKAAKAGAGLGGVPGVGGVAGAVVPPQAGVKKPGKVPVGL 146

QY 121 PGVYPGVLPGARPPGGVLPVPGVTPGAGVKKPAGVCGAFAGVPGVPGPGVPLGY 180
DB 147 PGVYPGVLPGARPPGGVLPVPGVTPGAGVKKPAGVCGAFAGVPGVPGPGVPLGY 206

QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVGAAGAKAGYPTGTGVPQAAAAAKAAKF 240

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## RESULT 2

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Q75MU5 PRELIMINARY; PRT; 757 AA.
ID Q75MU5;
AC Q75MU5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein ELN.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozeresky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris J.,
RA Strong C.M., Hou S., Tomlinson C., Rohlfsing T., Rock S.M.,
RA Kozlowicz-Reilly A., Leonard S., Dauphin-Kohlberg S.,
RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strommer J.P.,
RA Latreille P., Miller N., Johnson D., Mullis J.W., Spieth J.,
RA Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Cook L.L.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,
RA Simms E., Levy R., Clendinning J., Kaul R., Kent W.J., Furey T.S.,
RA Baerisch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005056; AAS07435.1; -.
DR InterPro; IPR001451; Hexapep.transf.

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DR InterPro; IPR003979; tropoelastin.  
DR PRINTS; PRO1500; TROPOLASTIN.  
DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 757 AA; 66106 MW; 2824F955D8360738 CRC64;  
Query Match 99.9%; Score 2676; DB 2; Length 757;  
Best Local Similarity 99.8%; Pred. No. 1.8e-99;  
Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GGVPGALPGGVPGGVPGVPGAGLGGALGGALGGKPLKPVPGGLAGLGGALGAGFAFPAVT 60  
Db 27 GGVPGALPGGVPGGVPGVPGAGLGGALGGALGGKPLKPVPGGLAGLGGALGAGFAFPAVT 86  
Qy 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVLSAGAVVPGAGVPGKVPKVGVL 120  
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVLSAGAVVPGAGVPGKVPKVGVL 146  
Qy 121 PGVYPGGVLPGARFPFGVGVLPFGVPTGAGVKPKAPGVGGAFAGIPGVGPFPGPQPGVPLGY 180  
Db 147 PGVYPGGVLPGARFPFGVGVLPFGVPTGAGVKPKAPGVGGAFAGIPGVGPFPGPQPGVPLGY 206  
Qy 181 PIKAPKLPGGYGLPYTTGKLPYGVPGGVVAGAAKAGAGYPTGTGTGVPQAAAAAATAAKAF 240  
Db 207 PIKAPKLPGGYGLPYTTGKLPYGVPGGVVAGAAKAGAGYPTGTGTGVPQAAAAAATAAKAF 266  
Qy 241 GAGAAGVLPVGGAGVPGVPGALPGIGIAGVGTTPAAAAAATAAKAAGAGLVPGG 300  
Db 267 GAGAAGVLPVGGAGVPGVPGALPGIGIAGVGTTPAAAAAATAAKAAGAGLVPGG 326  
Qy 301 PFGPGVGVPGAGVPGVPGAGIPVVPVPGAGIPVVPVPGVSPVSPVSPVSPVSPVSPVSPV 360  
Db 327 PFGPGVGVPGAGVPGVPGAGIPVVPVPGAGIPVVPVPGVSPVSPVSPVSPVSPVSPVSPV 386  
Qy 361 PGVGVGGIPYTYGVAGAGPFGVPGVGGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 420  
Db 387 PGVGVGGIPYTYGVAGAGPFGVPGVGGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 446  
Qy 421 AKAAKGVGTTPAAAAAATAAKAAGAGLVPGVPGVAGVPGVPGVAGVPGVPGVAGVPGV 480  
Db 447 AKAAKGVGTTPAAAAAATAAKAAGAGLVPGVPGVAGVPGVPGVAGVPGVPGVAGVPGV 506  
Qy 481 VGVAPGVGVPAGIPGGVAAAAAATAAKAAGAGLV 515  
Db 507 VGVAPGVGVPAGIPGGVAAAAAATAAKAAGLV 541  
RESULT 3  
ID AAS07435 PRELIMINARY; PRT; 757 AA.  
AC AAS07435;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein ELN.  
GN ELN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=22737993; PubMed=12853948;  
RA Hallier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,  
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,  
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,  
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,  
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,  
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,  
RA Ozerky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,  
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,  
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,  
RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strommatt C.,

RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,  
RA Wendt M.C., Yang S.P., Schultz B.R., Wallis J.M., Spieth J.,  
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,  
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,  
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,  
RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bub K.,  
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,  
RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,  
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,  
RA Bady S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,  
RA Waterston R.H., Wilson R.K.;  
RL "The DNA sequence of human chromosome 7.";  
RL Nature 424:157-164(2003).  
[2]  
SEQUENCE FROM N.A.  
RP Du H., Rohlfing T., Strong C.;  
RL "The sequence of Homo sapiens BAC clone CTB-51J22.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A.  
RP Waterston R.H.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
[4]  
SEQUENCE FROM N.A.  
RP Waterston R.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
[5]  
SEQUENCE FROM N.A.  
RP Wilson R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; ACO05056; AAS07435.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;  
Query Match 99.9%; Score 2676; DB 2; Length 757;  
Best Local Similarity 99.8%; Pred. No. 1.8e-99;  
Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GGVPGALPGGVPGGVPGVPGAGLGGALGGALGGKPLKPVPGGLAGLGGALGAGFAFPAVT 60  
Db 27 GGVPGALPGGVPGGVPGVPGAGLGGALGGALGGKPLKPVPGGLAGLGGALGAGFAFPAVT 86  
Qy 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVLSAGAVVPGAGVPGKVPKVGVL 120  
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVLSAGAVVPGAGVPGKVPKVGVL 146  
Qy 121 PGVYPGGVLPGARFPFGVGVLPFGVPTGAGVKPKAPGVGGAFAGIPGVGPFPGPQPGVPLGY 180  
Db 147 PGVYPGGVLPGARFPFGVGVLPFGVPTGAGVKPKAPGVGGAFAGIPGVGPFPGPQPGVPLGY 206  
Qy 181 PIKAPKLPGGYGLPYTTGKLPYGVPGGVVAGAAKAGAGYPTGTGTGVPQAAAAAATAAKAF 240  
Db 207 PIKAPKLPGGYGLPYTTGKLPYGVPGGVVAGAAKAGAGYPTGTGTGVPQAAAAAATAAKAF 266  
Qy 241 GAGAAGVLPVGGAGVPGVPGALPGIGIAGVGTTPAAAAAATAAKAAGAGLVPGG 300  
Db 267 GAGAAGVLPVGGAGVPGVPGALPGIGIAGVGTTPAAAAAATAAKAAGAGLVPGG 326  
Qy 301 PFGPGVGVPGAGVPGVPGAGIPVVPVPGAGIPVVPVPGVSPVSPVSPVSPVSPVSPVSPV 360  
Db 327 PFGPGVGVPGAGVPGVPGAGIPVVPVPGAGIPVVPVPGVSPVSPVSPVSPVSPVSPVSPV 386  
Qy 361 PGVGVGGIPYTYGVAGAGPFGVPGVGGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 420  
Db 387 PGVGVGGIPYTYGVAGAGPFGVPGVGGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 446  
Qy 421 AKAAKGVGTTPAAAAAATAAKAAGAGLVPGVPGVAGVPGVPGVAGVPGVPGVAGVPGV 480  
Db 447 AKAAKGVGTTPAAAAAATAAKAAGAGLVPGVPGVAGVPGVPGVAGVPGVPGVAGVPGV 506  
Qy 481 VGVAPGVGVPAGIPGGVAAAAAATAAKAAGLV 515  
Db 507 VGVAPGVGVPAGIPGGVAAAAAATAAKAAGLV 541

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RESULT 4
ELS_HUMAN
ID ELS_HUMAN STANDARD; PRT; 730 AA.
AC P1502; Q14233; Q14238;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Skin fibroblast;
RA Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Utito J.;
RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
RT recombinant cDNA library; further elucidation of alternative splicing
RT utilizing exon-specific oligonucleotides.";
RL J. Invest. Dermatol. 91:458-464(1988).
RN [3]
RP SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
RX TISSUE=Placenta;
RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
RA Rosenbloom J., Utito J.;
RT "Isolation and characterization of human elastin cDNAs, and age-
RT associated variation in elastin gene expression in cultured skin
RT fibroblasts.";
RL Lab. Invest. 58:270-277(1988).
RN [4]
RP SEQUENCE OF 603-730 FROM N.A.
RX TISSUE=Hippocampus, and Placenta;
RA Frangiskakis J.M., Ewart A.K., Morris C.A., Bertrand J.,
RA Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,
RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
RA Keating M.T.;
RT "LIM-kinase1 hemizygoty implicated in impaired visuospatial
RT constructive cognition.";
RL Cell 86:59-69(1996).
RN [5]
RP INVOLVEMENT IN CUTIS LAXA.
RX MEDLINE=99091639; PubMed=9873040;
RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
RT "Cutis laxa arising from frameshift mutations in exon 30 of the
RT elastin gene (ELN).";
RL J. Biol. Chem. 274:981-986(1999).
RN [6]
RP INVOLVEMENT IN SVAS.
RX PubMed=10942104;
RA Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
RA Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
RT "Isolated supravalvular aortic stenosis: functional haploinsufficiency
RT of the elastin gene as a result of nonsense-mediated decay.";
RL Hum. Genet. 106:577-588(2000).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
KW

```

CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=1;

CC IsoId=PI5502-1; Sequence=Displayed;

CC Name=2;

CC IsoId=PI5502-2; Sequence=VSP\_004243;

CC -!- PTM: The crosslinks are made of deaminated Lys.

CC -!- DISEASE: Defects in ELN are a cause of autosomal dominant cutis laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder characterized by loose, hyperextensible skin with decreased resilience and elasticity leading to a premature aged appearance. The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder diverticula, pulmonary artery stenosis and pyloric stenosis.

CC -!- DISEASE: Haploinsufficiency of ELN may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23.

CC -!- DISEASE: Defects in ELN are the cause of supravalvular aortic stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of the ascending aorta which can occur sporadically, as an autosomal dominant condition, or as one component of Williams-Beuren syndrome.

CC -----

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CC -----

CC EMBL; M17282; AAC98394.1; -

CC EMBL; M16983; AAC98394.1; JOINED.

CC EMBL; M17265; AAC98394.1; JOINED.

CC EMBL; M17266; AAC98394.1; JOINED.

CC EMBL; M17267; AAC98394.1; JOINED.

CC EMBL; M17268; AAC98394.1; JOINED.

CC EMBL; M17270; AAC98394.1; JOINED.

CC EMBL; M17271; AAC98394.1; JOINED.

CC EMBL; M17272; AAC98394.1; JOINED.

CC EMBL; M17273; AAC98394.1; JOINED.

CC EMBL; M17275; AAC98394.1; JOINED.

CC EMBL; M17276; AAC98394.1; JOINED.

CC EMBL; M17277; AAC98394.1; JOINED.

CC EMBL; M17278; AAC98394.1; JOINED.

CC EMBL; M17279; AAC98394.1; JOINED.

CC EMBL; M17280; AAC98394.1; JOINED.

CC EMBL; M17281; AAC98394.1; JOINED.

CC EMBL; M36860; AAA52382.1; -

CC EMBL; M24782; AAA53190.1; -

CC EMBL; U62292; AAB17544.1; -

CC EMBL; X15603; CAA33627.1; -

CC PIR; A32707; EAHU

CC HSSP; P50099; 1ZFU.

CC Genew; HGNC:3327; ELN.

CC MIM; 130160; -

CC MIM; 123700; -

CC MIM; 194050; -

CC MIM; 185500; -

CC GO; GO:0005578; C:extracellular matrix; TAS.

CC GO; GO:0005615; C:extracellular space; TAS.

CC GO; GO:0005201; F:extracellular matrix structural constituent; TAS.

CC GO; GO:0008283; P:cell proliferation; TAS.

CC GO; GO:0008015; P:circulation; TAS.

CC GO; GO:0009887; P:organogenesis; TAS.

CC GO; GO:0007585; P:respiratory gaseous exchange; TAS.

CC InterPro; IPR003979; tropoelastin.

CC PRINTS; PRO1500; TROP0ELASTIN.

CC Alternative splicing; Connective tissue; Repeat; Signal;

KW

KW Structural protein; Williams-Beuren syndrome.

FT SIGNAL 1 26  
FT CHAIN 27 730 Elastin.  
FT DISULFID 720 725 By similarity.  
FT VARSPLIC 472 477 Missing (in isoform 2).  
FT /FTID=VSP\_004243.  
SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;

Query Match 99.5%; Score 2667; DB 1; Length 730;

Best Local Similarity 98.8%; Pred. No. 4e-99; Indels 6; Gaps 1;  
Matches 515; Conservative 0; Mismatches 0;

QY 1 GGVPCAI PGVPGGVYFPCAGLGGAGLGGKPLKPVPGGLAGLGGAGLGAFFAVT 60  
Db 27 GGVPCAI PGVPGGVYFPCAGLGGAGLGGKPLKPVPGGLAGLGGAGLGAFFAVT 86  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLVGSAGAVVPPQAGVPGKVPVGL 120  
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLVGSAGAVVPPQAGVPGKVPVGL 146  
QY 121 PGVPGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFPQGVPLGY 180  
Db 147 PGVPGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFPQGVPLGY 206  
QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240  
Db 207 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 266  
QY 241 GAGAAGVLPVGGAGVPGVPCAIPIGIGIAGVGTTPAAAAAATAAKAYGAAAGLVPGG 300  
Db 267 GAGAAGVLPVGGAGVPGVPCAIPIGIGIAGVGTTPAAAAAATAAKAYGAAAGLVPGG 326  
QY 301 PGFGPGVVGVPAGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAAKAYKAGAR 360  
Db 327 PGFGPGVVGVPAGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAAKAYKAGAR 386  
QY 361 PGVGVGIGIPYGVGAGFPFGVPGVGGIPGVAGVPSVGGVPGVGGVPGVGSISPEAQAAA 420  
Db 387 PGVGVGIGIPYGVGAGFPFGVPGVGGIPGVAGVPSVGGVPGVGGVPGVGSISPEAQAAA 446  
QY 421 AKAAKYGVTTPAAAAAATAAKAF-----GLVPGVGVAPGVAGVPGVPGVGLAPG 474  
Db 447 AKAAKYGVTTPAAAAAATAAKAF-----GLVPGVGVAPGVAGVPGVPGVGLAPG 506  
QY 475 VGVAPGVGVAPGVAGVPGVPGVGGVAAAKAAKAAQAQLR 515  
Db 507 VGVAPGVGVAGVPGVPGVGGVAAAKAAKAAQAQLR 547

RESULT 5

Q7Z3F5  
ID Q7Z3F5 PRELIMINARY; PRT; 711 AA.  
AC Q7Z3F5  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein DKFp686F06102.  
GN Name=DKFp686F06102;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=Human fetal kidney;  
RC Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX537939; CAB97910.1;  
DR InterPro; IPR001451; Hexapep.transf.  
DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 711 AA; 61765 MW; 95B624A99B4A989B CRC64;

Query Match 99.2%; Score 2659.5; DB 2; Length 711;

Best Local Similarity 98.8%; Pred. No. 7.9e-99; Indels 5; Gaps 1;  
Matches 514; Conservative 0; Mismatches 1;

QY 1 GGVPCAI PGVPGGVYFPCAGLGGAGLGGKPLKPVPGGLAGLGGAGLGAFFAVT 60  
Db 27 GGVPCAI PGVPGGVYFPCAGLGGAGLGGKPLKPVPGGLAGLGGAGLGAFFAVT 86  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLVGSA-----GAVVPPQAGVPGKVP 115  
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLVGSAAPSVCAVVPQFAGVPGKVP 146  
QY 116 PGVGLPGVPGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFPQGP 175  
Db 147 PGVGLPGVPGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFPQGP 206  
QY 176 VPLGVPIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAK 235  
Db 207 VPLGVPIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAK 266  
QY 236 AAKEFGAGAGVLPVGGAGVPGVPGAIPIGIGIAGVGTTPAAAAAATAAKAYGAAAG 295  
Db 267 AAKEFGAGAGVLPVGGAGVPGVPGAIPIGIGIAGVGTTPAAAAAATAAKAYGAAAG 326  
QY 296 LVPGGPGFGVPGVPGAGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAAKAA 355  
Db 327 LVPGGPGFGVPGVPGAGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAAKAA 386  
QY 356 KYGARPGVGGIPYTYGVGAGFPFGVPGVGGIPGVAGVPSVGGVPGVGGVPGVGSISPEA 415  
Db 387 KYGARPGVGGIPYTYGVGAGFPFGVPGVGGIPGVAGVPSVGGVPGVGGVPGVGSISPEA 446  
QY 416 QAAAAKAAKYGVTTPAAAAAATAAKAAQFGLVPGVGVAGVPGVPGVAGVPGVGLAPG 475  
Db 447 QAAAAKAAKYGVTTPAAAAAATAAKAAQFGLVPGVGVAGVPGVPGVAGVPGVGLAPG 506  
QY 476 GVAPGVGVAGVPGVPGVGGVAAAKAAKAAQAQLR 515  
Db 507 GVAPGVGVAGVPGVPGVGGVAAAKAAKAAQAQLR 546

RESULT 6

Q15337  
ID Q15337 PRELIMINARY; PRT; 602 AA.  
AC Q15337  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Elastin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97358574; PubMed=9215670;  
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,  
RA Morris C.A., Keating M.T.;  
RT "Elastin point mutations cause an obstructive vascular disease,  
supravalvular aortic stenosis".  
RL Hum. Mol. Genet. 6:1021-1028 (1997).  
DR EMBL; U93037; AAB65620.1;  
DR EMBL; U93034; AAB65620.1; JOINED.  
DR EMBL; U93035; AAB65620.1; JOINED.  
DR EMBL; U93036; AAB65620.1; JOINED.  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro; IPR001451; Hexapep.transf.  
DR PRINTS; PR01500; TROPOLASTIN.  
DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
FT NON\_TER 1



analysis of cloned genomic and complementary DNA.";  
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684 (1987).

[2]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=87274906; PubMed=3038460;  
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,  
RA Rosenbloom J., Ornstein-Goldstein N.,  
RT "Structure of the 3' region of the human elastin gene: great abundance  
RT of Alu repetitive sequences and few coding sequences.";  
RL Connect. Tissue Res. 16:197-211 (1987).  
DR EMBL; M17282; AAC98393.1; JOINED.  
DR EMBL; M16983; AAC98393.1; JOINED.  
DR EMBL; M17265; AAC98393.1; JOINED.  
DR EMBL; M17266; AAC98393.1; JOINED.  
DR EMBL; M17267; AAC98393.1; JOINED.  
DR EMBL; M17268; AAC98393.1; JOINED.  
DR EMBL; M17271; AAC98393.1; JOINED.  
DR EMBL; M17272; AAC98393.1; JOINED.  
DR EMBL; M17273; AAC98393.1; JOINED.  
DR EMBL; M17275; AAC98393.1; JOINED.  
DR EMBL; M17276; AAC98393.1; JOINED.  
DR EMBL; M17277; AAC98393.1; JOINED.  
DR EMBL; M17278; AAC98393.1; JOINED.  
DR EMBL; M17279; AAC98393.1; JOINED.  
DR EMBL; M17281; AAC98393.1; JOINED.  
DR HSP; P50099; 12FJ.  
DR GO; GO:0005578; C:extracellular matrix; NAS.  
DR GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.  
DR InterPro; IPR001451; Hexapep.transf.  
DR PRINTS; PR01500; TROPOLASTIN.  
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.  
SQ SEQUENCE 687 AA; 59529 MW; 864068C4C8E3F88F\_CRC64;

Query Match 96.0%; Score 2571.5; DB 2; Length 687;  
Best Local Similarity 96.3%; Pred. No. 2.5e-95;  
Matches 496; Conservative 0; Mismatches 0; Indels 19; Gaps 1;  
QY 1 GGVPGAIPGGVPGGVFPYFGAGLGGALGGALGPGGKPLKPVPGGLAGLGGALGAGLGAFFAVT 60  
Db 27 GGVPGAIPGGVPGGVFPYFGAGLGGALGGALGPGGKPLKPVPGGLAGLGGALGAGLGAFFAVT 86  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKKPGKVPVGL 120  
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKKPGKVPVGL 146  
QY 121 PGVYPGVLPGARFPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 180  
Db 147 PGVYPGVLPGARFPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 206  
QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240  
Db 147 PGVYPGVLPGARFPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 206  
QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240  
Db 207 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 266  
QY 241 GAGAAGVLPGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 300  
Db 207 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 266  
QY 241 GAGAAGVLPGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 300  
Db 301 PGFPGVWGVPGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 360  
QY 267 GAGAAGVLPGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 326  
Db 301 PGFPGVWGVPGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 360  
QY 301 PGFPGVWGVPGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 360  
Db 327 GAGAAGVLPGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 386  
QY 361 PGVGVGGIPTYGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 420  
Db 327 PGFPGVWGVPGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 386  
QY 361 PGVGVGGIPTYGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 420  
Db 387 PGVGVGGIPTYGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 446  
QY 421 AKAAKYGVGTPTAAAAAATAAKAFGLVPGVAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 480  
Db 447 AKAAKY-----GLVPGVAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 522  
QY 481 VGAVPGVAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 515  
Db 488 VGAVPGVAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 522

RESULT 10  
Q6P0L4  
ID Q6P0L4 PRELIMINARY; PRT; 658 AA.  
AC Q6P0L4;

RESULT 9  
Q7Z316  
ID Q7Z316 PRELIMINARY; PRT; 687 AA.  
AC Q7Z316;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)  
DE Hypothetical protein DKFZp686O21208 (Fragment).  
GN Name=DKFZp686O21208;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
RA Han M., Wiemann S.,  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538199; CAD98065.1; -.  
DR InterPro; IPR001451; Hexapep.transf.  
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 687 AA; 59847 MW; 79232A191DC1F10F\_CRC64;

Query Match 93.3%; Score 2500.5; DB 2; Length 687;  
Best Local Similarity 94.2%; Pred. No. 1.7e-92;  
Matches 485; Conservative 0; Mismatches 1; Indels 29; Gaps 2;  
QY 1 GGVPGAIPGGVPGGVFPYFGAGLGGALGGALGPGGKPLKPVPGGLAGLGGALGAGLGAFFAVT 60  
Db 37 GGVPGAIPGGVPGGVFPY-----ALGPGGKPLKPVPGGLAGLGGALGAGLGAFFAVT 86  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKKPGKVPVGL 120  
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKKPGKVPVGL 146  
QY 121 PGVYPGVLPGARFPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 180  
Db 147 PGVYPGVLPGARFPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 206  
QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240  
Db 207 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 266  
QY 241 GAGAAGVLPGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 300  
Db 267 GAGAAGVLPGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 326  
QY 301 PGFPGVWGVPGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 360  
Db 327 PGFPGVWGVPGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 386  
QY 361 PGVGVGGIPTYGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 420  
Db 387 PGVGVGGIPTYGVGAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 446  
QY 421 AKAAKYGVGTPTAAAAAATAAKAFGLVPGVAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 480  
Db 447 AKAAKY-----GLVPGVAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 522  
QY 481 VGAVPGVAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 515  
Db 488 VGAVPGVAGVPGVPGAGIPGIGGIAGVGTPTAAAAAATAAKAF 522



Mon Nov 22 12:42:43 2004

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DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE ELN protein.
GN Name=ELN;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065566; AAH65566.1; -.
DR InterPro; IPR001451; Hexapep trans.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN 1.
SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 90.0%; Score 2411.5; DB 2; Length 658;
Best Local Similarity 93.2%; Pred. No. 5.6e-89;
Matches 468; Conservative 0; Mismatches 1; Indels 33; Gaps 2;

QY 1 GGVPGAIPGVGGVPGVPGAGLGGALGGALGGKPLKFPVGGLAGAGLGAFAFPAVT 60
DB 27 GGVPGAIPGVGGVPGVPGAGLGGALGGALGGKPLKFPVGGLAGAGLGAFAFPAVT 86

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGVVPQPGKPKVGVGL 120
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGVVPQPGKPKVGVGL 146

QY 121 PGVPGGVLPGARFPFGVGLPGVPTGAGVKPAPGVGGAGAGIPGVGGPQGVPLGY 180
DB 147 PGVPGGVLPGARFPFGVGLPGVPTGAGVKPAPGVGGAGAGIPGVGGPQGVPLGY 206

QY 181 PIKAPKLPKPGYGLPYTTGKLPYGYGGVAGAGKAGYPTGTGVPQAAAAAAXKAF 240
DB 207 PIKAPKLP-----GYGGVAGAGAGKAGYPTGTGVPQAAAAAAXKAF 252

QY 241 GAGAAGVLPVGGAGVPGVPGAIPIGGIAGVGTAAAAAAXKAYGAAAGVPGG 300
DB 253 GAGAAGVLPVGGAGVPGVPGAIPIGGIAGVGTAAAAAAXKAYGAAAGVPGG 312

QY 301 PGFGPGVWPGVAGVPGVPGAGIPVVPAGIPGAAPGVVSPVSPVSPVSPVSPVSPV 360
DB 313 PGFGPGVWPGVAGVPGVPGAGIPVVPAGIPGAAPGVVSPVSPVSPVSPVSPV 372
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60,770 full-length cDNAs.<sup>8</sup>;  
Nature 420:563-573 (2002).  
[4]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Thymus;  
MEDLINE=20499374; PubMed=11042159;  
R Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
Kanno H., Akizawa J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
Fujiwara K., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
"RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer";  
Genome Res. 10:1617-1630 (2000).  
[5]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Thymus;  
MEDLINE=20530913; PubMed=11076861;  
R Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
Kanno H., Akizawa J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
Fujiwara K., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
"RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer";  
Genome Res. 10:1751-1771 (2000).  
[6]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Thymus;  
R Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
Kato H., Kawai J., Kohji Y., Kondo S., Konno H., Kouda M., Koya S.,  
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
Tagawa A., Takahashi F., Takaki-Akanira S., Takeda Y., Tanaka T.,  
Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
[7]  
SEQUENCE FROM N.A.  
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
MEDLINE=23386257; PubMed=12477932;  
R Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzyszynski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[8]  
SEQUENCE FROM N.A.  
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
R Strausberg R.,  
Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
R EMBL; AK041860; BAC31084.1; -;  
R EMBL; BC051649; AAH51649.1; -;  
R MGD; MGI:95317; Eln.  
R GO; GO:0007519; P:myogenesis; IMP.

60,770 full-length cDNAs.";  
Nature 420:563-573 (2002).  
[4]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Thymus;  
MEDLINE=20499374; PubMed=11042159;  
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Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
"RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer";  
Genome Res. 10:1617-1630 (2000).  
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SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Thymus;  
MEDLINE=20530913; PubMed=11076861;  
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Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
Kato H., Kawai J., Kohji Y., Kondo S., Konno H., Kouda M., Koya S.,  
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
Tagawa A., Takahashi F., Takaki-Akanira S., Takeda Y., Tanaka T.,  
Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
[7]  
SEQUENCE FROM N.A.  
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
MEDLINE=23386257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzyszynski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[8]  
SEQUENCE FROM N.A.  
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
Strausberg R.;  
Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
RA EMBL; AK041860; BAC31084.1; -;  
RA EMBL; BC051649; AAH51649.1; -;  
RA MGD; MGI:95317; Eln.  
RA GO; GO:0007519; P:myogenesis; IMP.

"Use of an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human chromosome 7.";

CC -!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.

CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.

CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.

CC -!- PTM: The crosslinks are made of deaminated Lys.

CC -----

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CC -----

DR EMBL; U08210; AAA80155.1; -.

DR PIR; A55721; EAMS.

DR MGD; MGI:95317; Eln.

DR InterPro; IPR003979; tropoelastin.

DR PRINTS; PR01500; TROPOELASTIN.

CC KW Connective tissue; Repeat; Signal; Structural protein.

FT SIGNAL 1 27 Potential.

FT CHAIN 28 860 Elastin.

FT DISULFID 850 855 By similarity.

CC SQ SEQUENCE 860 AA; 71955 MW; 0C0BESA5AE1EDD7F1 CRC64;

Query Match 64.5%; Score 1728.5; DB 1; Length 860;

Best Local Similarity 64.0%; Pred. No. 1e-61;

Matches 395; Conservative 16; Mismatches 63; Indels 143; Gaps 26;

QY 1 GVGPGALPGGVGGVFFPGAGLIGAL--GGCALPGGKPLKP-----VPGGLAGAG 48

DB 32 GAVPGGLPGGVGGVYYPGAGIGLGGGGALPGGKPKPGAGLIGTFGAGPGLGGAG 91

QY 49 LGAGLGAFFAVTFF--GALVPGGVADAAAYK-AAKAGAGLGGVPGV----- 92

DB 92 PGAGLGAFFAGTFFGAGALVPGGAAGAAAYKAAAKAGAGLGGVGGVGGVGGVGGV 151

QY 93 -----GGLGVSAVAWFPQPGAGV---KPGKVPQVGLPGVY 124

DB 152 GVGVPGGVGGVGGVGGVGGIGGLGVSTGAVVPQVGAGIGAGGKPKVPGVGLPGVY 211

QY 125 PGGVLP--GARPPGVGLPVPPTAGVKPKAPGVGAFAGIPGVGPFPGQPQVPLGYPI 182

DB 212 PGGVLPPTGARPPGVGLPVPPTGTGKAPKPGGGAFSGIPGVGPFQGFPLGYPI 271

QY 183 KAPKLPGGVGLPYTTGKLPYGYPGGVAGAAGKAGYPTGTGVGPQAAAAAATAAKTGA 242

DB 272 KAPKLPGGVGLPYTNGKLPV---GVAGAGGKAGYPTGTGVGSQAAAAA--KAAKYGA 324

QY 243 GAAGVLPVGGGAGVPGVPGAIPGIGIAGVGTPTAAAAAATAAKYGAAGLVPGGPG 302

DB 325 GGAGVLPVGGGGIPGGAIPAIPGIGIAGAGTFAAAAAATAAKYGAAGLVPGGPG 384

QY 303 FGPVGVVPGVAGVPGV-GVPG-AGIPVPGAGIPGNAV---PGVVPSPAAATAAKYKY 357

DB 385 -----VRLPGAGIPGVGGIPGVGGIPGVGGIPGVGGIPGVGGIPGVGGIPGVGGIP 439

QY 358 GARPVGVGGIPTYGVAGGFFPGFVGVGGI PGVAGVSPGVGGVGGVGGVGGVGGVGGV 417

DB 440 GARGGV---GIPTYGVAGGFFPGYGVGAGA-----GLGGA-----SP-AAA 476

QY 418 AAAAATAKY-----GVGTPTAAAAATAAKA-A 442

DB 477 AAAAATAKYTAGAGAGALGGLVPGAVPGALPGAVPAVPGAGGVPGAGTPTAAAAATAAKA 536

QY 443 AQFGLVPGGVAPGVGVPAGVGVAP---GVGLPAGVGVAPGVGVPAGVGVAP-GIGPGGV 498

DB 537 AKAGLPGVGGVPGV-GV--GVGGIPGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 590













Db 566 GGLAPGVAGVPGV--GGPAAAAKAAKAA 592

RESULT 28  
Q9BDZ0 PRELIMINARY; PRT; 172 AA.

ID Q9BDZ0 AC Q9BDZ0; 2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Elastin (Fragment).  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=21621082; PubMed=11751201;  
RA Sekhon H.S., Keller J.A., Prokocil B.J., Martin E.L., Spindel E.R.;  
RT "Maternal nicotine exposure upregulates collagen gene expression in fetal monkey lung. Association with alpha7 nicotinic acetylcholine receptors.";  
RT Am. J. Respir. Cell Mol. Biol. 26:31-41(2002).  
RL EMBL; AF230927; AAK14974.1; -.  
FT NON TER 1  
FT NON TER 172  
FT NON TER 172  
SQ SEQUENCE 172 AA; 15224 MW; 4980EF4C5AF3330B CRC64;

Query Match 29.8%; Score 797.5; DB 2; Length 172;  
Best Local Similarity 90.1%; Pred. No. 4.3e-25;  
Matches 155; Conservative 0; Mismatches 6; Indels 11; Gaps 2;

QY 33 GKPLKPVGGLAGLAGGALGAFPAVTPFGALPVGGVADAAAAYKAAGAGLGVP-- 90  
Db 1 GKPLKPVGGLAGTGLGAGLGAFFAGFAGALPVGGVADAAAAYKAAGAGLGVPV 60

QY 91 -----GVGGLGVSAAGAVPPGAGVKPKVGVGLPGVPGVLP--GARFPGVGLP 141  
Db 61 GGIGGVGGVGLGVSTGAVVPPGAGVKPKVGVGLPGVPGVLPDGTGARFPGVGLP 120

QY 142 GVPTGAGVKPKAPGVGGAFAGIPGVGPFGPVPGLGYPIKAPKLPGGYGL 193  
Db 121 GVPTGAGVKPKAPGVGGAFAGIPGVGPFGVPGVGLPYPIKAPKLPGGYGL 172

RESULT 29  
Q9BIT7 PRELIMINARY; PRT; 1953 AA.

ID Q9BIT7 AC Q9BIT7; 2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Major ampullate spidroin 2-like protein (Fragment).  
OS Nephila inaurata madagascariensis.  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Araneomorphae; Entelegynae; Araneioidea; Tetragrathidae; Nephila.  
OX NCBI\_TaxID=115969;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=21179804; PubMed=11283372;  
RA Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.;  
RT "Extreme diversity, conservation, and convergence of spider silk fibroin sequences.";  
RT Science 291:2603-2605(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gatesy J.E., Hayashi C.Y.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF350276; AAK30605.1; -.  
FT NON TER 1  
FT NON TER 1  
FT NON TER 1953  
FT NON TER 1953

SQ SEQUENCE 1953 AA; 159383 MW; C82B4DACD043CBDC CRC64;

Query Match 22.9%; Score 614; DB 2; Length 1953;  
Best Local Similarity 33.8%; Pred. No. 4.1e-17;  
Matches 233; Conservative 16; Mismatches 237; Indels 204; Gaps 33;

QY 2 GVPGAI-----PGGVPGGFVYPGA-----GLGALGGGALGPGKPLKVPVPGLAGAG 48  
Db 688 GGPGGAAAAAAGPGGPGQGPGGAAAAAAGSGPGGYGPGQQGFGG-----PGAAAAA 741  
QY 49 LG-----AGLCAPFAVTFPGALVPGGVADAAAAYKAAGAGLGCV----- 89  
Db 742 AGRGPGGYGQGGPGGPGGAAAAAAGPGGYGPGQQGPGGAAAAAAGRGPGGYGPGQQG 799  
QY 90 PGVGLGVSAAGAVPPGAGVKPKV-----PQVGLPGVYPGVGLPGARFPGVGLPGV-- 143  
Db 800 PGRSAAAAAAGRGPG--GYGPGQQGPGGAAAAAAGPGGYGPGQQGPGGAAAAAASAGR 858  
QY 144 -PTGAGVKFKAPGVGAFAFIPGVGPF--GP---OPGVLP-LGYPIKAPKLPGGYG----- 192  
Db 859 GPGGYGPGQGPGGSGAAAAAAGRGPGGYGPGQQGPGGAAAAAAGRGPGGYGPGQQG 918  
QY 193 -----LPYTITGLPYGYGFG-----GVAGAAGKAGYPTGTGVPQAAAAAAXAA 237  
Db 919 PQGGPGGSGAAAAAAGRGPGGYGPGQQGPGGAAAAAAGPGGYGPGQQGPGGAAAAA 978  
QY 238 AKFGAGAAGVLPGVGAGVPGVPGAIPGIG-----GIAGVCTPAAAAAAXAAKAYG 291  
Db 979 ---GSGPGGYGPGQQGPGGAAAAAAGRGPGGYGPGQQGPGGAAAAAAGRGPGGYG 1035  
QY 292 -----AAAGLVPGG-----PGFPGVVGVPGA 313  
Db 1036 PQGGPGQGPGSGAAAAAAGRGPGGYGPGQQGPGGAAAAAAGPGGYGPGQQG-PGA 1094  
QY 314 -----GVFPGVPGVPGVGCISPEAOAAAAAAXAAKAYGVSP-----EAAAKA 350  
Db 1095 AAAAAAAGRGPGGYGPGQQGPGGAAAAAAGRG--PGGYGPGQQGPGGPGCAAAA 1153  
QY 351 AKAAXYG-ARPGVGVTIYGVGAGF-----PGFVGVCVGP 390  
Db 1154 AAGPGGYGPGQQGPGGAAAAAAGSGAGGYGPGQQGPGGAAAAAAGPGGYGPGQQG-PG 1212  
QY 391 VAGVPSVGGVPGVPGVGCISPEAOAAAAAAXAAKAYGVST--PAAAAAK----- 437  
Db 1213 AAAAAAGSGPGGYGPGQQGPGGSSAAAAAAGPCRYGPGQQGPGGAAAAAAGSGPGGYG 1272  
QY 438 -----AAAKAAOFGLVPGVGAFF-----VGVAPGVVAPGVGLAFGV 477  
Db 1273 GQQGPGGPGHAAAAAAGRGPG--GYGPGQQGPGGAAAAAAGPG--GYGPG-QQGPGAAA 1329  
QY 478 APGVGVAPGVGAFF--IGPGVAAAAAKSAA 506  
Db 1330 AAAAGSGPG-GYGPGQQGPGGAAAAAAGAAAAA 1358

RESULT 30  
Q9BIU9 PRELIMINARY; PRT; 651 AA.

ID Q9BIU9 AC Q9BIU9; 2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Flagelliform silk protein (Fragment).  
GN Name=Flag;  
OS Argiope trifasciata (Banded garden spider).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Araneomorphae; Entelegynae; Araneioidea; Araneidae; Argiope.  
OX NCBI\_TaxID=156845;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=21179804; PubMed=11283372;  
RA Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.;  
RX "Extreme diversity, conservation, and convergence of spider silk FT

```
RT      fibroin sequences.";
RL      Science 291:2603-2605(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Gatesy J.E., Hayashi C.Y.;
RL      Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF350264; AAK30593.1; -.
FT      NON_TER
SQ      SEQUENCE 651 AA; 52360 MW; 77CEEC8757DE48DA CRC64;

Query Match      22.4%; Score 600.5; DB 2; Length 651;
Best Local Similarity 38.5%; Pred. No. 7e-17;
Matches 225; Conservative 17; Mismatches 201; Indels 141; Gaps 39;

QY      2  GVPGALPGVPGGVFPVPGAGLALG--GGALPGGKPLKFPVPGLAGAGLGA-----G 52
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      2  GGPGA--GGAGAGGVPG--GFGPGGFGGAGGPGG-----PGGPGAGGAGGAGGLYG 52
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      53  LGAFPAVTPPGAL-----VPG--GVADAAAYKAAKAGAGLGGV-----PGVGGLGV 97
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      53  PGAGGLYGPGLYGGGAGVFCAPGASGRAGGICGAAGAGAGGVPGGVSGGAGGAGG 112
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      98  SAGAVVPGAGVKPGVGLPGVPGGLPGVPGVPGVPGVPGV--PTGAGVFKAPG 155
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      113  SGTVVESVSVGGAG--PGAG--GVGPGGVPGGVGPG-----GIYFGGAG--GLYGF 162
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      156  VGGAF-----AGTPGVPGPGPQGVPLGYPKAPKLPGGYGLPVTGKLPYGYGPG--GV 209
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      163  AGGAFPGGGAGAPG--GPGGPGGPGPGG-----LGGVGGAGTGG-----GVPGAGG 210
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      210  AGAGKAGVPTGTGVPQAAAAAATAKFGAGAGVLPVGGAGVPGV--PGAIPGIGG 268
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      211  VPGSGAG-----GTGPVSVSVTVGGAG--GPGAGG--PGAGGAGAGGVGPGFGGPGG 262
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      269  IAGVGTAAAAAATAKAAKYAAAGLV--PGGPG-----FGPGVVGVPG----- 312
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      354  AAKYGARPEV-----GVGGIPYGVGAGGFPFGVGVGIPGVAG-----VPSVG 398
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      379  GG-FGGRGGPGGPGGPGGPRFGGAAGAGAGAGGVGPGGVGGAGGSGSVTVVESVSVG 437
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      399  GV--PGVGVPGVGISPEAQAAAAAATAKAAKYGVTFPAAAAAATAKAAQFGLVPGVVAPG 456
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      438  GAGGPGAGGVPGGVGP-----GGVPGGIYPPGAGGLYGPAGGA--FGSGGGAG--APG 490
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      457  VGVAPGVGVAPGVGLAPGVGA--PGVGVAPGVGVAPGIGPGGVA 499
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      491  GPGGPGGPGGPG--GLGGGVGAGTGGGVGPGV---GVGPGGGA 530
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: November 19, 2004, 16:36:48  
Job time : 108.124 secs



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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:37:11 ; Search time 8.00262 Seconds  
(without alignments)  
2168.321 Million cell updates/sec

Title: US-09-743-818A-72

Perfect score: 253

Sequence: 1 AAAGLAGIPGLGVGVGPG.....LGVGAGVPGFAGAGDEGVR 49

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :				Published Applications_AA.*			
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*				2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*			
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*				4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*			
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*				6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*			
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*				8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*			
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*				10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*			
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*				12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*			
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*				16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*			
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*				20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*			
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1	253	100.0	731	10	US-09-964-662-1	Sequence 1, Appl	
2	212	83.8	617	14	US-10-104-047-2915	Sequence 2915, Ap	
3	212	83.8	663	15	US-10-108-260A-2477	Sequence 2477, Ap	
4	212	83.8	692	15	US-10-210-172-40	Sequence 40, Appl	
5	212	83.8	711	15	US-10-210-172-38	Sequence 38, Appl	
6	212	83.8	730	10	US-09-961-403-8	Sequence 8, Appl	
7	149	58.9	60	8	US-08-806-029-24	Sequence 24, Appl	
8	149	58.9	64	8	US-08-806-029-18	Sequence 18, Appl	
9	149	58.9	64	14	US-10-117-931-14	Sequence 14, Appl	
10	149	58.9	244	16	US-10-800-179-27	Sequence 27, Appl	
11	149	58.9	246	16	US-10-800-179-26	Sequence 26, Appl	
12	149	58.9	246	16	US-10-800-179-28	Sequence 28, Appl	
13	149	58.9	312	8	US-08-806-029-34	Sequence 34, Appl	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

14	149	58.9	378	14	US-10-117-931-26	Sequence 26, Appl
15	149	58.9	696	8	US-08-806-029-36	Sequence 36, Appl
16	149	58.9	696	15	US-10-441-965-23	Sequence 23, Appl
17	149	58.9	750	8	US-08-806-029-25	Sequence 25, Appl
18	149	58.9	768	8	US-08-806-029-35	Sequence 35, Appl
19	149	58.9	884	14	US-10-117-931-15	Sequence 15, Appl
20	149	58.9	889	8	US-08-806-029-19	Sequence 19, Appl
21	149	58.9	905	16	US-10-800-179-31	Sequence 31, Appl
22	149	58.9	1002	14	US-10-117-931-25	Sequence 25, Appl
23	149	58.9	1011	14	US-10-096-986-94	Sequence 94, Appl
24	149	58.9	1038	16	US-10-800-179-30	Sequence 30, Appl
25	149	58.9	1465	14	US-10-096-986-74	Sequence 74, Appl
26	149	58.9	2055	14	US-10-096-986-81	Sequence 81, Appl
27	149	58.9	2257	14	US-10-096-986-82	Sequence 82, Appl
28	148.5	58.7	65	14	US-10-117-931-9	Sequence 9, Appl
29	148	58.5	884	16	US-10-800-179-25	Sequence 25, Appl
30	146	57.7	696	15	US-10-441-965-21	Sequence 21, Appl
31	141	55.7	54	14	US-10-117-931-24	Sequence 24, Appl
32	139.5	55.1	60	14	US-10-117-931-29	Sequence 29, Appl
33	139.5	55.1	128	8	US-08-806-029-13	Sequence 13, Appl
34	139.5	55.1	936	14	US-10-117-931-30	Sequence 30, Appl
35	139.5	55.1	953	8	US-08-806-029-14	Sequence 14, Appl
36	137	54.2	64	15	US-10-441-965-20	Sequence 20, Appl
37	136.5	54.0	62	14	US-10-117-931-33	Sequence 33, Appl
38	136.5	54.0	64	14	US-10-117-931-4	Sequence 4, Appl
39	136.5	54.0	64	14	US-10-117-931-5	Sequence 5, Appl
40	136.5	54.0	966	14	US-10-117-931-34	Sequence 34, Appl
41	136	53.8	832	8	US-08-806-029-27	Sequence 27, Appl
42	136	53.8	936	8	US-08-806-029-26	Sequence 26, Appl
43	136	53.8	988	8	US-08-806-029-28	Sequence 28, Appl
44	136	53.8	1056	8	US-08-806-029-29	Sequence 29, Appl
45	134	53.0	972	8	US-08-806-029-30	Sequence 30, Appl
46	134	53.0	1024	8	US-08-806-029-31	Sequence 31, Appl
47	134	53.0	1040	8	US-08-806-029-32	Sequence 32, Appl
48	131.5	52.0	148	9	US-09-837-969A-14	Sequence 14, Appl
49	131.5	52.0	148	9	US-09-841-321A-14	Sequence 14, Appl
50	131.5	52.0	745	9	US-09-837-969A-38	Sequence 38, Appl
51	131.5	52.0	745	9	US-09-841-321A-38	Sequence 38, Appl
52	129.5	51.2	45	9	US-09-837-969A-59	Sequence 59, Appl
53	129.5	51.2	45	9	US-09-841-321A-59	Sequence 59, Appl
54	128.5	50.8	450	9	US-09-812-382-6	Sequence 6, Appl
55	128.5	50.8	1305	16	US-10-720-025-62	Sequence 62, Appl
56	127.5	50.4	111	9	US-09-837-969A-13	Sequence 13, Appl
57	127.5	50.4	111	9	US-09-841-321A-13	Sequence 13, Appl
58	127.5	50.4	782	9	US-09-837-969A-37	Sequence 37, Appl
59	127.5	50.4	782	9	US-09-841-321A-37	Sequence 37, Appl
60	127.5	50.4	2003	9	US-09-837-969A-34	Sequence 34, Appl
61	127.5	50.4	2003	9	US-09-841-321A-34	Sequence 34, Appl
62	127	50.2	485	16	US-10-720-025-21	Sequence 21, Appl
63	127	50.2	1169	8	US-08-806-029-33	Sequence 33, Appl
64	126.5	50.0	1580	16	US-10-720-025-52	Sequence 52, Appl
65	126.5	50.0	1780	16	US-10-720-025-59	Sequence 59, Appl
66	126.5	50.0	2030	15	US-10-720-025-53	Sequence 53, Appl
67	126	49.8	780	15	US-10-441-965-19	Sequence 19, Appl
68	126	49.8	780	16	US-10-800-179-19	Sequence 19, Appl
69	125.5	49.6	40	14	US-10-096-986-43	Sequence 43, Appl
70	125.5	49.6	50	9	US-09-812-382-3	Sequence 3, Appl
71	125.5	49.6	50	9	US-09-837-969A-29	Sequence 29, Appl
72	125.5	49.6	50	9	US-09-841-321A-29	Sequence 29, Appl
73	125.5	49.6	100	9	US-09-812-382-7	Sequence 7, Appl
74	125.5	49.6	106	9	US-09-837-969A-53	Sequence 53, Appl
75	125.5	49.6	106	9	US-09-841-321A-53	Sequence 53, Appl
76	125.5	49.6	111	9	US-09-837-969A-58	Sequence 58, Appl
77	125.5	49.6	111	9	US-09-841-321A-58	Sequence 58, Appl
78	125.5	49.6	605	9	US-09-837-969A-40	Sequence 40, Appl
79	125.5	49.6	605	9	US-09-841-321A-40	Sequence 40, Appl
80	125.5	49.6	605	14	US-10-356-088-62	Sequence 62, Appl
81	125.5	49.6	605	16	US-10-799-326-62	Sequence 62, Appl
82	125.5	49.6	750	16	US-10-720-025-41	Sequence 41, Appl
83	125.5	49.6	760	16	US-10-720-025-23	Sequence 23, Appl
84	125.5	49.6	859	14	US-10-096-986-77	Sequence 77, Appl
85	125.5	49.6	960	16	US-10-720-025-24	Sequence 24, Appl
86	125.5	49.6	1200	16	US-10-720-025-42	Sequence 42, Appl





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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 2.20393 Seconds  
(without alignments)  
2139.188 Million cell updates/sec

Title: US-09-743-818A-72  
Perfect score: 253  
Sequence: 1 AAGAGAGIPGLGVGVGPG.....LGVGAGVPGFAGAGEGVRR 49

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: PIR 79:.\*  
2: PIR1:.\*  
3: PIR2:.\*  
4: PIR3:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253	100.0	792	1 EAHU	elastin precursor,
2	193	76.3	860	1 EAMS	elastin precursor,
3	189	74.7	747	1 EABO	elastin precursor,
4	181	71.5	864	1 EART	elastin precursor,
5	168.5	66.6	770	2 S59623	tropoelastin - she
6	126.5	50.0	784	2 A26601	elastin precursor
7	125.5	49.6	907	2 A45560	elastin precursor
8	107	42.3	127	2 E82734	sporozoite surface
9	103.5	40.9	108	2 G86252	hypothetical prote
10	97	38.3	151	2 T08002	hypothetical prote
11	96	37.9	100	2 T7558	glycine-rich prote
12	96	37.9	158	2 T08957	glycine-rich prote
13	95.5	37.7	212	2 E86179	hypothetical prote
14	95	37.5	108	1 S01844	fibroin - silkworm
15	94.5	37.4	130	2 T04048	hypothetical prote
16	94.5	37.4	16	2 AC1064	outer membrane fim
17	94	37.2	129	2 T17530	glycine-rich prote
18	94	37.2	505	2 T04143	CLB1 protein - tom
19	93	36.8	185	2 JC4085	glycine-rich cutic
20	93	36.8	1901	2 F70806	hypothetical glyci
21	92	36.4	223	2 B96506	hypothetical prote
22	92	36.4	1733	1 B45344	probable nuclear a
23	92	36.4	1958	2 B40505	hypothetical prote
24	91.5	36.2	129	2 A24255	chorion class A pr
25	91	36.0	259	2 T17889	glycine-rich prote
26	91	36.0	523	2 AH2907	signal recognition
27	91	36.0	554	2 H97682	glycine-rich cell
28	90.5	35.8	162	2 S56703	hypothetical prote
29	89	35.2	143	2 S43071	hypothetical prote

30	89	35.2	171	2 T43959	hypothetical prote
31	89	35.2	510	2 T50526	CalB protein - Ara
32	88.5	35.0	208	2 S23463	cuticular protein
33	88.5	35.0	532	2 T35119	probable aminotran
34	88.5	35.0	1147	1 MWAXIB	myosin heavy chain
35	88	34.8	924	2 B41359	potassium channel
36	88	34.8	924	2 S12746	potassium channel
37	87.5	34.6	162	2 C85356	glycine-rich prote
38	87.5	34.6	3190	2 T13828	CREB-binding prote
39	87	34.4	384	1 A26099	glycine-rich cell
40	87	34.4	641	1 QOBE31	nuclear antigen EB
41	86.5	34.2	627	2 T04562	hypothetical prote
42	86	34.0	186	2 S28021	rab18 protein - Ar
43	85.5	33.8	234	2 G95989	hypothetical glyci
44	85.5	33.8	298	2 E95286	hypothetical prote
45	84.5	33.4	107	2 B85356	glycine-rich prote
46	84.5	33.4	419	2 G70602	hypothetical prote
47	84	33.2	139	2 T33968	hypothetical prote
48	84	33.2	839	2 C85046	probable reverse t
49	84	33.2	1240	2 T04193	hypothetical prote
50	82.5	32.6	129	2 T03861	glycine-rich prote
51	82	32.4	180	2 T49530	related to glycine
52	82	32.4	205	2 T07959	probable cell wall
53	82	32.4	338	1 KXNU	glycine-rich cell
54	82	32.4	486	1 KRXL	keratin 3, type I,
55	81.5	32.2	131	2 T05837	hypothetical prote
56	81.5	32.2	149	2 T18758	hypothetical prote
57	81	32.0	53	2 A42627	cement precursor p
58	81	32.0	603	2 A70770	hypothetical glyci
59	81	32.0	1215	2 T32734	myosin-IA - Acanth
60	80.5	31.8	447	2 G84687	probable disease r
61	80.5	31.8	496	2 H70839	hypothetical glyci
62	80	31.6	200	2 B86181	hypothetical prote
63	80	31.6	419	1 KRXL2B	keratin, 64K type
64	80	31.6	420	2 A49642	transcription fact
65	80	31.6	543	2 F70726	hypothetical glyci
66	80	31.6	1328	2 G84519	probable retroelem
67	80	31.6	1596	2 A33106	neurogenic locus m
68	79.5	31.4	87	2 T14302	glycine-rich cell
69	79.5	31.4	1489	2 D70807	hypothetical glyci
70	79	31.2	70	2 A83982	hypothetical prote
71	79	31.2	300	2 A39112	merozoite 45K surf
72	79	31.2	302	2 A39615	probable RNA bindi
73	79	31.2	496	2 S68160	hypothetical glyci
74	79	31.2	882	2 B70812	hypothetical prote
75	79	31.2	1758	2 T29350	collagen alpha 2(I
76	79	31.2	1759	2 T29351	probable large gly
77	79	31.2	1772	2 T36105	hypothetical prote
78	78.5	31.0	479	2 F70573	elastin - bovine (
79	78	30.8	76	2 I45885	circumsporozoite p
80	78	30.8	201	2 T00799	phosphatidylinosit
81	78	30.8	351	1 OZ2QKU	dnax-type molecula
82	78	30.8	490	2 T09084	hypothetical glyci
83	78	30.8	686	2 A49242	chorion class A pr
84	78	30.8	778	2 F70963	probable beta-1,3
85	77.5	30.6	119	1 JAAO92	glycine-rich prote
86	77.5	30.6	228	2 D86416	probable keratin 1
87	77.5	30.6	396	2 T49109	polyketide synthas
88	77.5	30.6	473	4 A33652	hypothetical prote
89	77.5	30.6	1616	2 G70668	glycine-rich prote
90	77	30.4	102	2 E85189	hypothetical prote
91	77	30.4	210	2 JQ1060	hypothetical prote
92	77	30.4	1844	2 T51890	related to Nup98-N
93	76.5	30.2	191	2 T23594	hypothetical prote
94	76.5	30.2	214	2 T23593	hypothetical prote
95	76.5	30.2	255	2 S84777	hypothetical prote
96	76.5	30.2	271	2 S34666	glycine-rich prote
97	76.5	30.2	354	4 A27071	cytoplasmic male s
98	76.5	30.2	399	2 T18566	hypothetical prote
99	76.5	30.2	447	2 B96720	hypothetical prote
100	76.5	30.2	3716	2 E70969	probable PPE prote

Mon Nov 22 12:42:44 2004

## ALIGNMENTS

## RESULT 1

EAHU  
 elastin precursor, long splice form - human  
 N:Alternate names: tropoelastin  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Jun-1990 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: A32707; A33705; A30524; A53891  
 R:Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987  
 A:Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA  
 A:Reference number: A32707; MUID:87289668; PMID:3039501  
 A:Accession: A32707  
 A:Molecule type: mRNA  
 A:Residues: 1-500, 507-792 <IND>  
 A:Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948  
 R:Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.  
 J. Biol. Chem. 264, 8887-8891, 1989  
 A:Title: Characterization of the complete human elastin gene. Delineation of unusual features  
 A:Reference number: A33705; MUID:99255358; PMID:2722804  
 A:Accession: A33705  
 A:Molecule type: DNA  
 A:Residues: 1-27 <BAS>  
 A:Cross-references: GB:J04821; NID:gl82052; PIDN:AAA52379.1; PID:g553276  
 R:Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.  
 J. Invest. Dermatol. 91, 458-464, 1988  
 A:Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA library  
 A:Reference number: A30524; MUID:89009960; PMID:3171221  
 A:Accession: A30524  
 A:Molecule type: mRNA  
 A:Residues: 1-453, 483-617, 651-792 <PAZ>  
 A:Cross-references: ENBL:M36860; NID:gl82061; PIDN:AAA52382.1; PID:gl82062  
 A:Note: this sequence represents a composite of several splice forms  
 R:Fazio, M.J.; Olsen, D.R.; Kuhlvanemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U  
 Lab. Invest. 58, 270-277, 1988  
 A:Title: Isolation and characterization of human elastin cDNAs, and age-associated variations  
 A:Reference number: A53891; MUID:88156138; PMID:2831431  
 A:Accession: A53891  
 A:Molecule type: mRNA  
 A:Residues: 164-453, 483-500, 507-617, 651-792 <PAZ>  
 A:Cross-references: GB:M24782; NID:gl82063; PIDN:AAA53190.1; PID:gl82064  
 C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix  
 C:Genetics: GDB:ELN  
 A:Gene: GDB:ELN  
 A:Cross-references: GDB:119107; OMIM:130160  
 A:Map position: 7q11.23-7q11.23  
 C:Superfamily: elastin  
 C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-792/Product: elastin #status predicted <MAT>  
 F:782-787/Disulfide bonds: #status predicted  
 Query Match 100.0%; Score 253; DB 1; Length 792;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGGAGPGLGVGVPGLGVGAGVPGFGLGVGAGVPGFAGAGVRR 49  
 |||||  
 Db 577 AAAGLGGAGPGLGVGVPGLGVGAGVPGFGLGVGAGVPGFAGAGVRR 625

## RESULT 2

EAWS  
 elastin precursor - mouse  
 N:Alternate names: tropoelastin  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Aug-1995 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: A55721  
 R:Wyder, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.  
 Genomics 23, 125-131, 1994

A:Title: Use of an intron length polymorphism to localize the tropoelastin gene to mouse chromosome 12  
 A:Reference number: A55721; MUID:95130069; PMID:7829060  
 A:Accession: A55721  
 A:Molecule type: mRNA  
 A:Residues: 1-860 <WID>  
 A:Cross-references: UNIPROT:P54320; GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274  
 C:Genetics:  
 A:Map position: 5  
 C:Superfamily: elastin  
 C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
 F:1-27/Domain: signal sequence #status predicted <SIG>  
 F:28-860/Product: elastin #status predicted <MAT>  
 F:850-855/Disulfide bonds: #status predicted  
 Query Match 76.3%; Score 193; DB 1; Length 860;  
 Best Local Similarity 81.4%; Pred. No. 2.1e-10;  
 Matches 35; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAAGLGGAGPGLGVGVPGLGVGAGVPGFGLGVGAGVPGFAGAGVRR 43  
 |||||  
 Db 608 AAAGLGGAGVPGFAGAGVPGFAGAGVPGFAGAGVPGFAGAGVRR 650

RESULT 3  
 BABO  
 elastin precursor, splice form a - bovine  
 N:Alternate names: tropoelastin  
 N:Contains: elastin precursor, splice form b; elastin precursor, splice form c  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 08-Jun-1989 #sequence\_revision 28-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: A31865; A26728; C26728; A25886  
 R:Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams  
 Biochemistry 28, 2365-2370, 1989  
 A:Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing  
 A:Reference number: A31865; MUID:89274159; PMID:2543440  
 A:Accession: A31865  
 A:Molecule type: DNA  
 A:Residues: 1-27 <YEH>  
 A:Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:g340504; PIDN:AAA307  
 R:Raju, K.; Anwar, R.A. 5755-5762, 1987  
 J. Biol. Chem. 262, 5755-5762, 1987  
 A:Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of complementary DNAs  
 A:Reference number: A92640; MUID:87194772; PMID:3032943  
 A:Accession: A26728  
 A:Molecule type: mRNA  
 A:Residues: 1, 'RS', 4-11, 'E', 13-636, 'V', 638-747 <RAJ>  
 A:Cross-references: GB:J02717; NID:gl63019; PIDN:AAA30503.1; PID:gl63020  
 A:Accession: B26728  
 A:Molecule type: mRNA  
 A:Residues: 1, 'RS', 4-11, 'E', 13-225, 240-636, 'V', 638-747 <RA2>  
 A:Cross-references: GB:K03505; NID:gl63025; PIDN:AAA30505.1; PID:gl63026  
 A:Accession: C26728  
 A:Molecule type: mRNA  
 A:Residues: 1, 'RS', 4-11, 'E', 13-225, 260-636, 'V', 638-747 <RA3>  
 A:Cross-references: GB:K03506; NID:gl63027; PIDN:AAA30506.1; PID:gl63028  
 R:Cicila, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbloom, J.  
 Biochemistry 24, 3075-3080, 1985  
 A:Title: Structure of the 3' portion of the bovine elastin gene  
 A:Reference number: A22343; MUID:85280426; PMID:2992576  
 A:Accession: A22343  
 A:Molecule type: DNA  
 A:Residues: 613-747 <CIC>  
 A:Cross-references: GB:M20415  
 R:Rosenbloom, J.  
 Lab. Invest. 51, 605-623, 1984  
 A:Title: Biology of disease: Elastin: Relation of protein and gene structure to diseases  
 A:Reference number: I45885; MUID:85059254; PMID:6150137  
 A:Accession: I45886  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 678-683, 685-747 <ROS>  
 A:Cross-references: GB:M31898; NID:gl63015; PIDN:AAA96417.1; PID:gl63018  
 R:Brown, P.L.; Mecham, L.; Tidale, C.; Mecham, R.P.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 9.90699 Seconds  
(without alignments)  
2845.805 Million cell updates/sec

Title: US-09-743-818A-72

Perfect score: 253

Sequence: 1 AAGAGGAGPGLGVGVGVRG.....LGVGAGVPGFAGAGDEGVRR 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	253	100.0	757	2	Q14234	Q14234	homo sapien
2	253	100.0	757	2	Q75MU5	Q75MU5	homo sapien
3	253	100.0	757	2	AA07435	AA07435	homo sapi
4	245	96.8	635	2	O15336	O15336	homo sapien
5	212	83.8	258	2	Q9UMF5	Q9UMF5	homo sapien
6	212	83.8	570	2	Q6ZWI6	Q6ZWI6	homo sapien
7	212	83.8	570	2	BAC85506	BAC85506	homo sapi
8	212	83.8	643	2	Q8NB14	Q8NB14	homo sapien
9	212	83.8	687	2	Q14235	Q14235	homo sapien
10	212	83.8	711	2	Q72316	Q72316	homo sapien
11	212	83.8	711	2	Q72316	Q72316	homo sapien
12	212	83.8	730	1	EL5_HUMAN	EL5_HUMAN	homo sapien
13	208	82.2	472	2	Q8N2G0	Q8N2G0	homo sapien
14	205	81.0	679	2	Q28097	Q28097	homo sapien
15	204	80.6	602	2	O15337	O15337	homo sapien
16	204	80.6	658	2	Q6P014	Q6P014	homo sapien
17	204	80.6	658	2	RAH65566	RAH65566	homo sapi
18	199	78.7	650	2	Q28099	Q28099	homo sapien
19	199	78.7	666	2	Q28096	Q28096	homo sapien
20	199	78.7	707	2	Q28098	Q28098	homo sapien
21	193	76.3	810	2	Q9ESZ9	Q9ESZ9	mus taurus
22	193	76.3	860	1	EL5_MOUSE	EL5_MOUSE	mus musculus
23	193	76.3	860	1	Q8C918	Q8C918	mus musculus
24	189	74.7	747	1	EL5_BOVIN	EL5_BOVIN	mus musculus
25	181	71.5	864	1	EL5_RAT	EL5_RAT	mus musculus
26	131.5	52.0	1092	2	Q964R2	Q964R2	rattus norv
27	126.5	50.0	907	1	EL5_CHICK	EL5_CHICK	gallus gall
28	125.5	49.6	907	2	Q26575	Q26575	thellieria a
29	117	46.2	196	2	Q8P2F2	Q8P2F2	methanosarc
30	115	45.5	559	2	Q6ZUN2	Q6ZUN2	homo sapien
31	115	45.5	559	2	BAC86188	BAC86188	homo sapi

32	112	44.3	301	2	Q01927	Q01927	phytophthor
33	111	43.9	194	2	Q6PY85	Q6PY85	kukulcania
34	111	43.9	194	2	AAT08432	AAT08432	kukulcani
35	110	43.5	117	2	Q88913	Q88913	thermoprote
36	110	43.5	343	2	Q01914	Q01914	phytophthor
37	109.5	43.3	897	2	Q60294	Q60294	agelenopsis
38	109.5	43.3	897	2	AAT08436	AAT08436	agelenopsis
39	108	42.7	850	2	Q83SR9	Q83SR9	salmonella
40	107	42.3	93	2	Q819Q8	Q819Q8	arabidopsis
41	107	42.3	120	2	Q88914	Q88914	thermoprote
42	107	42.3	127	2	Q9PEK3	Q9PEK3	thermoprote
43	105.5	41.7	723	2	Q9N7Q7	Q9N7Q7	xyella fas
44	105	41.5	5263	1	FB0CB_BOMMO	FB0CB_BOMMO	thellieria l
45	104.5	41.3	279	2	Q6C3L2	Q6C3L2	bombyx mori
46	103.5	40.9	108	2	Q65397	Q65397	yarrowia li
47	103	40.7	658	2	Q9JL61	Q9JL61	arabidopsis
48	101.5	40.1	184	2	Q701T9	Q701T9	mus musculu
49	101.5	40.1	476	2	Q80890	Q80890	anopheles g
50	101	39.9	99	2	Q7X186	Q7X186	herpesvirus
51	101	39.9	613	2	Q9NCN0	Q9NCN0	oryza sativ
52	100.5	39.7	169	2	Q8WRP0	Q8WRP0	penaeus van
53	100.5	39.7	1032	2	Q6XLI7	Q6XLI7	penaeus van
54	100.5	39.7	1032	2	AA048569	AA048569	rattus norv
55	100	39.5	786	2	Q75GM7	Q75GM7	penaeus van
56	100	39.5	786	2	AAT01369	AAT01369	oryza sativ
57	99	39.1	153	2	Q9BUQ3	Q9BUQ3	oryza sat
58	99	39.1	158	2	Q94668	Q94668	plasmodium
59	99	39.1	167	2	Q9QY1	Q9QY1	plasmodium
60	99	39.1	175	2	Q9GQX5	Q9GQX5	plasmodium
61	99	39.1	195	2	Q25715	Q25715	plasmodium
62	99	39.1	195	2	Q25948	Q25948	plasmodium
63	99	39.1	223	2	Q25788	Q25788	plasmodium
64	99	39.1	618	2	Q90W76	Q90W76	oncorhynch
65	99	39.1	760	2	Q6PY84	Q6PY84	kukulcania
66	99	39.1	760	2	AAT08433	AAT08433	kukulcani
67	98	38.7	205	2	Q25946	Q25946	plasmodium
68	98	38.7	347	2	Q01916	Q01916	phytophthor
69	97	38.3	151	2	Q22600	Q22600	onobrychis
70	97	38.3	224	2	Q7QHT5	Q7QHT5	anopheles g
71	97	38.3	267	1	PM27_STRPU	PM27_STRPU	strongyloce
72	97	38.3	988	2	Q17434	Q17434	nephila cla
73	96.5	38.1	163	2	Q8WRP1	Q8WRP1	penaeus van
74	96	37.9	59	2	Q225H5	Q225H5	mus musculu
75	96	37.9	87	2	Q225H6	Q225H6	mus musculu
76	96	37.9	100	2	Q89403	Q89403	paramecium
77	96	37.9	158	2	Q9SZD2	Q9SZD2	arabidopsis
78	96	37.9	216	2	Q9U099	Q9U099	plasmodium
79	96	37.9	515	2	Q7XAL6	Q7XAL6	oryza sativ
80	96	37.9	592	2	Q90W75	Q90W75	oncorhynch
81	95.5	37.7	103	2	Q225D6	Q225D6	homo sapien
82	95.5	37.7	163	2	Q8WRP2	Q8WRP2	penaeus van
83	95.5	37.7	163	2	Q8WRP4	Q8WRP4	penaeus van
84	95.5	37.7	163	2	Q8WRP5	Q8WRP5	penaeus van
85	95.5	37.7	212	2	Q23018	Q23018	arabidopsis
86	95	37.5	135	2	Q9BJP4	Q9BJP4	plasmodium
87	95	37.5	158	2	Q9GQX4	Q9GQX4	plasmodium
88	95	37.5	524	2	Q8AWB2	Q8AWB2	lampetra fl
89	95	37.5	922	2	Q43367	Q43367	mytilus edu
90	94.5	37.4	382	2	Q9SV88	Q9SV88	arabidopsis
91	94.5	37.4	382	2	Q6DIN1	Q6DIN1	xenopus tro
92	94.5	37.4	581	2	Q7V2M3	Q7V2M3	prochloroco
93	94.5	37.4	838	2	Q8Z0Z7	Q8Z0Z7	salmonella
94	94	37.2	129	2	Q89375	Q89375	paramecium
95	94	37.2	152	2	Q9BJJ5	Q9BJJ5	plasmodium
96	94	37.2	437	2	Q8VK97	Q8VK97	mycobacteri
97	94	37.2	505	2	Q48645	Q48645	lycopersico
98	94	37.2	1488	2	Q9GUB5	Q9GUB5	galleria me
99	93.5	37.0	503	2	Q9HEH4	Q9HEH4	neurospora
100	93	36.8	185	2	O18507	O18507	tenebrio mo

ALIGNMENTS

GN	Name=ELN;
OS	Homo sapiens (Human);
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE=22737999; PubMed=12853948;
RX	Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA	Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA	Fyfe G.A., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA	Powell K.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA	Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA	Vandrun A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA	Ozersky P., Bielik L., Scott K., Holmes A., Harkins R., Harris A.,
RA	Strong C.M., Hou S., Tomlinson C., Daughin-Kohlberg S.,
RA	Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA	Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strommatt C.,
RA	Latreille P., Miller N., Johnson D., Murray J., Spieth J.,
RA	Wend M.C., Yang S.P., Schultz B.R., Wallis J.W., Piepho J.,
RA	Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA	Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA	Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA	Gillett W., Zhou Y., James R., Phelps K., Iadonoto S., Bubbs K.,
RA	Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Firey T.S.,
RA	Baertsch R.A., Brent M.R., Keibler E., Flieck P., Bork P., Suyama M.,
RA	Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA	Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RT	"The DNA sequence of human chromosome 7.";
RL	Nature 424:157-164(2003).
[2]	
RN	SEQUENCE FROM N.A.
RP	Waterston R.;
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
[3]	
RN	SEQUENCE FROM N.A.
RA	Wilson R.;
RL	Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AC005056; AAC07435.1; -.
DR	InterPro; IPRO01451; Hexapep.transf.
DR	Prints; PRO1500; TROPOLASTIN.
DR	PRINTS; PRO1500; TROPOLASTIN.
DR	PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
	Query Match 100.0%; Score 253; DB 2; Length 757;
	Best Local Similarity 100.0%; Pred.No. 1.1e-12;
	Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AAAGLGAGTGGGCGVPGVGAGVPGVGLGVGAGVPGVGFAGADEGVRR 49 
Db	542 AAAGLGAGTGGGCGVPGVGAGVPGVGLGVGAGVPGVGFAGADEGVRR 590 
RESULT 3	
AAS07435	PRELIMINARY; PRT; 757 AA.
ID	AAS07435
AC	AAS07435
DT	02-MAR-2004 (TrEMBLrel. 27, Created)
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein ELN.
GN	ELN.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE=22737999; PubMed=12853948;
RX	Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA	Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA	Fyfe G.A., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA	Powell K.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA	Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA	Vandrun A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA	Ozersky P., Bielik L., Scott K., Holmes A., Harkins R., Harris A.,
RA	Strong C.M., Hou S., Tomlinson C., Daughin-Kohlberg S.,
RA	Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA	Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strommatt C.,
RA	Latreille P., Miller N., Johnson D., Murray J., Spieth J.,
RA	Wend M.C., Yang S.P., Schultz B.R., Wallis J.W., Piepho J.,
RA	Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA	Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA	Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA	Gillett W., Zhou Y., James R., Phelps K., Iadonoto S., Bubbs K.,
RA	Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Firey T.S.,
RA	Baertsch R.A., Brent M.R., Keibler E., Flieck P., Bork P., Suyama M.,
RA	Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA	Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RT	"The DNA sequence of human chromosome 7.";
RL	Nature 424:157-164(2003).
[2]	
RN	SEQUENCE FROM N.A.
RP	Waterston R.;
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
[3]	
RN	SEQUENCE FROM N.A.
RA	Wilson R.;
RL	Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AC005056; AAC07435.1; -.
DR	InterPro; IPRO01451; Hexapep.transf.
DR	Prints; PRO1500; TROPOLASTIN.
DR	PRINTS; PRO1500; TROPOLASTIN.
DR	PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 757 AA; 66136 MW; 23B7E5B9AF85CA8 CRC64;
	Query Match 100.0%; Score 253; DB 2; Length 757;
	Best Local Similarity 100.0%; Pred.No. 1.1e-12;
	Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AAAGLGAGTGGGCGVPGVGAGVPGVGLGVGAGVPGVGFAGADEGVRR 49 
Db	542 AAAGLGAGTGGGCGVPGVGAGVPGVGLGVGAGVPGVGFAGADEGVRR 590 
RESULT 2	
Q75MU5	PRELIMINARY; PRT; 757 AA.
ID	Q75MU5
AC	Q75MU5
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein ELN.
GN	ELN.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE=87289668; PubMed=3038460;
RX	Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA	Rosenbloom J., Ornstein-Goldstein N.; Sheppard P., Anderson N.,
RA	Indik Z., Yeh H., Peltonen L., Rosenbloom J.;
RA	Rosenbloom J.C., Peltonen L., Rosenbloom J.

RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,  
 RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,  
 RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,  
 RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,  
 RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,  
 RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,  
 RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,  
 RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,  
 RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strommatt C.,  
 RA Latrelle P., Miller N., Johnson D., Murray J., Woessner J.P.,  
 RA Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,  
 RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,  
 RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,  
 RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,  
 RA Glanville W., Zhou Y., James R., Phelps K., Iadonato S., Bub K.,  
 RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,  
 RA Baertsch R.A., Brent M.R., Keibler E., Fliscek P., Bork P., Suyama M.,  
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,  
 RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,  
 RA Waterston R.H., Wilson R.K.;  
 RT "The DNA sequence of human chromosome 7.";  
 RL Nature 424:157-164 (2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Du H., Rohlfing T., Strong C.;  
 RT "The sequence of Homo sapiens BAC clone CTB-51J22.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.H.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Wilson R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC005056; AAS07435.1; --  
 KW Hypothetical protein.  
 SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;  
 Query Match 100.0%; Score 253; DB 2; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 49  
 Db 542 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 590  
 RESULT 4  
 O15336 ID O15336 PRELIMINARY; PRT; 635 AA.  
 AC O15336;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Elastin (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97358574; PubMed=9215670;  
 RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,  
 RA Morris C.A., Keating M.T.;  
 RT "Elastin point mutations cause an obstructive vascular disease,  
 RT supravalvular aortic stenosis.";  
 RL Hum. Mol. Genet. 6:1021-1028 (1997).  
 DR EMBL; U93037; AAB65621.1; --  
 Query Match 83.8%; Score 212; DB 2; Length 258;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-10;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGA 41  
 Db 76 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGA 116  
 RESULT 6  
 Q6ZMJ6 ID Q6ZMJ6 PRELIMINARY; PRT; 570 AA.  
 AC Q6ZMJ6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DR EMBL; U93034; AAB65621.1; JOINED.  
 DR EMBL; U93035; AAB65621.1; JOINED.  
 DR EMBL; U93036; AAB65621.1; JOINED.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
 DR InterPro; IPR001451; Hexapep transf.  
 DR PRINTS; PR01500; TROPOLASTIN.  
 DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
 FT NON\_TER 1 635  
 FT NON\_TER 635  
 SQ SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;  
 Query Match 96.8%; Score 245; DB 2; Length 635;  
 Best Local Similarity 98.0%; Pred. No. 4.3e-12;  
 Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 49  
 Db 549 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 597

## RESULT 5

Q9UMF5 ID Q9UMF5 PRELIMINARY; PRT; 258 AA.  
 AC Q9UMF5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Elastin (Fragment).  
 GN Name=ELN;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96411691; PubMed=8812460;  
 RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,  
 RA Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,  
 RA Koop B.F., Tsui L.-C.;  
 RT "Identification of genes from a 500-kb region at 7q11.23 that is  
 RT commonly deleted in Williams syndrome patients.";  
 RL Genomics 36:328-336 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20458868; PubMed=11003705;  
 RA Martindale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,  
 RA Duronio V., Koop B.F.;  
 RT "Comparative genomic sequence analysis of the Williams syndrome region  
 RT (LIMK1-RFC2) of human chromosome 7q11.23.";  
 RL Mamm. Genome 11:890-898 (2000).  
 DR EMBL; U63721; AAC13884.1; --  
 DR InterPro; IPR001451; Hexapep transf.  
 DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
 FT NON\_TER 1 635  
 FT NON\_TER 635  
 SQ SEQUENCE 258 AA; 21990 MW; C39BF7298D0E05D2 CRC64;  
 Query Match 83.8%; Score 212; DB 2; Length 258;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-10;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGA 41  
 Db 76 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGA 116  
 RESULT 6  
 Q6ZMJ6 ID Q6ZMJ6 PRELIMINARY; PRT; 570 AA.  
 AC Q6ZMJ6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
Hypothetical protein FLJ16246.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,  
Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,  
Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,  
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
Yamaashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,  
Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,  
Masuho Y., Nagai K., Isogai T.;  
Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
EMBL; AK12731; BAC85506.1; -  
InterPro: IPR001451; Hexapep transf.  
InterPro: IPR003979; tropoelastin.  
PRINTS: PR01500; TROPOELASTIN.  
PROSITE: PS00101; HEXAPEP\_TRANSFERS; UNKNOWN 1.  
SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;  
Query Match 83.8%; Score 212; DB 2; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGAGTGGVGVGVPGLGVGAGVPGVGAGVPGFGA 41  
|||||  
406 AAAGLGAGTGGVGVGVPGLGVGAGVPGVGAGVPGVGAGVPGFGA 446  
DE  
RESULT 7  
BAC85506 PRELIMINARY; PRT; 570 AA.  
ID BAC85506  
AC BAC85506;  
DT 02-MAR-2004 (TREMBLrel. 27, Created)  
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
DE CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin  
DE gene.  
DE Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,  
Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,  
Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,  
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
Yamaashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,  
Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,  
Masuho Y., Nagai K., Isogai T.;  
"NEDO human cDNA sequencing project";  
Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
EMBL; AK12731; BAC85506.1; -  
SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;  
Query Match 83.8%; Score 212; DB 2; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGAGTGGVGVGVPGLGVGAGVPGVGAGVPGVGAGVPGFGA 41  
|||||  
406 AAAGLGAGTGGVGVGVPGLGVGAGVPGVGAGVPGVGAGVPGFGA 446  
Db  
RESULT 8  
Q9NBI4

```

DR EMBL; M17276; AAC98393.1; JOINED.
DR EMBL; M17277; AAC98393.1; JOINED.
DR EMBL; M17278; AAC98393.1; JOINED.
DR EMBL; M17279; AAC98393.1; JOINED.
DR EMBL; M17281; AAC98393.1; JOINED.
DR HSP; P50099; 12FJ.
DR GO; GO:000578; C:extracellular matrix; NAS.
DR GO; GO:003023; F:extracellular matrix constituent conferring. . .; NAS.
DR InterPro; IPR001451; Hexapep transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 687 AA; 59529 MW; 864068C4C859F88F CRC64;

Query Match      83.8%; Score 212; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41
Db 523 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 563

RESULT 10
Q72316 PRELIMINARY; PRT; 687 AA.
AC Q72316
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686O21208 (Fragment).
GN Name=DKFZp686O21208;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538199; CAD9065.1; -.
DR InterPro; IPR001451; Hexapep transf.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 687 AA; 59847 MW; 79232A19DC1F10F CRC64;

Query Match      83.8%; Score 212; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41
Db 523 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 563

RESULT 11
Q723F5 PRELIMINARY; PRT; 711 AA.
AC Q723F5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686F06102.
GN Name=DKFZp686F06102;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human fetal kidney;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537939; CAD97910.1; -.
DR InterPro; IPR001451; Hexapep transf.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 711 AA; 61765 MW; 95B624A99B4A989B CRC64;

Query Match      83.8%; Score 212; DB 2; Length 711;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41
Db 547 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 587

RESULT 12
ELS_HUMAN
ID ELS_HUMAN STANDARD; PRT; 730 AA.
AC P1502; Q14233; Q14238;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684 (1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Skin fibroblast;
RX MEDLINE=89009960; PubMed=3171221;
RA Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Utito J.;
RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
RT recombinant cDNA library; further elucidation of alternative splicing
RT utilizing exon-specific oligonucleotides.";
RL J. Invest. Dermatol. 91:458-464 (1988).
RN [3]
RP SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
RC TISSUE=Placenta;
RX MEDLINE=88156138; PubMed=2831431;
RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
RA Rosenbloom J., Utito J.;
RT "Isolation and characterization of human elastin cDNAs, and age-
RT associated variation in elastin gene expression in cultured skin
RT fibroblasts.";
RL Lab. Invest. 58:270-277 (1988).
RN [4]
RP SEQUENCE OF 603-730 FROM N.A.
RC TISSUE=Hippocampus, and Placenta;
RX MEDLINE=96291399; PubMed=8689688;
RA Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
RA Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,
RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
RA Keating M.T.;
RT "LIM-kinase1 hemizyosity implicated in impaired visuospatial
RT constructive cognition.";
RL Cell 86:59-69 (1996).
RN [5]
RP INVOLVEMENT IN CUTIS LAXA.

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RX MEDLINE=99091639; PubMed=9873040;  
 RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;  
 RT "Cutis laxa arising from frameshift mutations in exon 30 of the  
 RT elastin gene (ELN).";  
 RL J. Biol. Chem. 274:981-986(1999).  
 RN [6]  
 RP INVOLVEMENT IN SVAS.  
 RX PubMed=10942104;  
 RA Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,  
 RA Munich A., Eyekens B., Gewillig M., Devriendt K., Boyd C.D.;  
 RA "Isolated supravalvular aortic stenosis: functional haploinsufficiency  
 RT of the elastin gene as a result of nonsense-mediated decay.";  
 RL Hum. Genet. 106:577-588(2000).  
 CC -!- FUNCTION: Major structural protein of tissues such as aorta and  
 CC nuchal ligament, which must expand rapidly and recover completely.  
 CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together  
 CC into an extensible 3D network.  
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1;  
 CC IsoId=P15502-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P15502-2; Sequence=VSP\_004243;  
 CC -!- PTM: The crosslinks are made of deaminated Lys.  
 CC -!- DISEASE: Defects in ELN are a cause of autosomal dominant cutis  
 CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder  
 CC characterized by loose, hyperextensible skin with decreased  
 CC resilience and elasticity leading to a premature aged appearance.  
 CC The skin changes are often accompanied by extracutaneous  
 CC manifestations, including pulmonary emphysema, bladder  
 CC diverticula, pulmonary artery stenosis and pyloric stenosis.  
 CC -!- DISEASE: Haploinsufficiency of ELN may be the cause of certain  
 CC cardiovascular and musculo-skeletal abnormalities observed in  
 CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare  
 CC developmental disorder and a contiguous gene deletion syndrome  
 CC involving genes from chromosome band 7q11.23.  
 CC -!- DISEASE: Defects in ELN are the cause of supravalvular aortic  
 CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of  
 CC the ascending aorta which can occur sporadically, as an autosomal  
 CC dominant condition, or as one component of Williams-Beuren  
 CC syndrome.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M17282; AAC98394.1; JOINED.  
 CC EMBL; M16983; AAC98394.1; JOINED.  
 CC EMBL; M17265; AAC98394.1; JOINED.  
 CC EMBL; M17266; AAC98394.1; JOINED.  
 CC EMBL; M17267; AAC98394.1; JOINED.  
 CC EMBL; M17268; AAC98394.1; JOINED.  
 CC EMBL; M17270; AAC98394.1; JOINED.  
 CC EMBL; M17271; AAC98394.1; JOINED.  
 CC EMBL; M17272; AAC98394.1; JOINED.  
 CC EMBL; M17273; AAC98394.1; JOINED.  
 CC EMBL; M17275; AAC98394.1; JOINED.  
 CC EMBL; M17276; AAC98394.1; JOINED.  
 CC EMBL; M17277; AAC98394.1; JOINED.  
 CC EMBL; M17278; AAC98394.1; JOINED.  
 CC EMBL; M17279; AAC98394.1; JOINED.  
 CC EMBL; M17280; AAC98394.1; JOINED.  
 CC EMBL; M17281; AAC98394.1; JOINED.  
 CC EMBL; M36860; AAA52382.1; -  
 CC EMBL; M24782; AAA53190.1; -  
 CC EMBL; U62292; AAB17544.1; -  
 CC EMBL; X15603; CAA33627.1; -

DR PIR; A32707; EAHU.  
 DR HSP; P50099; 1ZFU.  
 DR Genew; HGNC:3327; ELM.  
 DR MIM; 130160; -  
 DR MIM; 123700; -  
 DR MIM; 194050; -  
 DR MIM; 185500; -  
 DR GO; GO:0005578; C:extracellular matrix; TAS.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.  
 DR GO; GO:0008283; P:cell proliferation; TAS.  
 DR GO; GO:0008015; P:circulation; TAS.  
 DR GO; GO:0009887; P:organogenesis; TAS.  
 DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOELASTIN.  
 DR KW Alternative splicing; Connective tissue; Repeat; Signal;  
 KW Structural protein; Williams-Beuren syndrome.  
 FT SIGNAL 1 26 Elastin.  
 FT CHAIN 27 730 By similarity.  
 FT DISULFID 720 725 Missing (in isoform 2).  
 FT VARSPPLIC 472 477 Missing (in isoform 2).  
 FT FTId=VSP\_004243.  
 FT SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;  
 Query Match 83.8%; Score 212; DB 1; Length 730;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGGAGIPGLGVGVPGVLGVGAGVPGVGVGAGVPGFGA 41  
 DB 548 AAAGLGGAGIPGLGVGVPGVLGVGAGVPGVGVGAGVPGFGA 588  
 RESULT 13  
 Q8N2G0 PRELIMINARY; PRT; 472 AA.  
 ID Q8N2G0;  
 AC Q8N2G0;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein PSEC0191.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Whole embryo;  
 RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,  
 RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,  
 RA Nagahari K., Sugano S., Isogai T.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK075494; BAC11651.1; -  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
 DR InterPro; IPR001451; Hexapep transf.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOELASTIN  
 DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.  
 FT NON\_TER 472 472  
 SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;  
 Query Match 82.2%; Score 208; DB 2; Length 472;  
 Best Local Similarity 97.6%; Pred. No. 3.1e-09;  
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AAAGLGGAGIPGLGVGVPGVLGVGAGVPGVGVGAGVPGFGA 41  
 DB 316 AAAGLGGAGIPGLGVGVPGVLGVGAGVPGVGVGAGVPGFGA 356  
 RESULT 14





Mon Nov 22 12:42:44 2004

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SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;
Query Match 80.6%; Score 204; DB 2; Length 658;
Best Local Similarity 97.6%; Pred. No. 8.3e-09;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 41
    |||||
Db 494 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 534

RESULT 17
AAH65566 PRELIMINARY; PRT; 658 AA.
ID AAH65566
AC AAH65566;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE ELN protein.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065566; AAH65566.1; 5DAFC00D16A2F94E CRC64;
SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 80.6%; Score 204; DB 2; Length 658;
Best Local Similarity 97.6%; Pred. No. 8.3e-09;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 41
    |||||
Db 494 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 534

RESULT 18
Q28099 PRELIMINARY; PRT; 650 AA.
ID Q28099
AC Q28099;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Elastin-CBEL1; NCBI gi: 163003 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30499.1; JOINED.
DR EMBL; M11422; AAA30499.1; JOINED.
DR EMBL; M19366; AAA30499.1; JOINED.
DR EMBL; M19368; AAA30499.1; JOINED.
DR EMBL; M19369; AAA30499.1; JOINED.
DR EMBL; M19370; AAA30499.1; JOINED.
DR EMBL; M19371; AAA30499.1; JOINED.
DR EMBL; M22771; AAA30499.1; JOINED.
DR EMBL; M22772; AAA30499.1; JOINED.
DR EMBL; M22773; AAA30499.1; JOINED.
DR EMBL; M22774; AAA30499.1; JOINED.
DR EMBL; M22775; AAA30499.1; JOINED.
DR EMBL; M22988; AAA30499.1; JOINED.
DR EMBL; M23010; AAA30499.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001979; Tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR NON TER 1
SQ SEQUENCE 650 AA; 55373 MW; CD21ABB3E9076AD7 CRC64;

Query Match 78.7%; Score 199; DB 2; Length 650;
Best Local Similarity 92.7%; Pred. No. 2.1e-08;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 41
    |||||
Db 468 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 508

RESULT 19
Q28096 PRELIMINARY; PRT; 666 AA.
ID Q28096
AC Q28096;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Elastin-CBEL3; NCBI gi: 163005 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;

```

RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,  
 RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;  
 RT "Sequence variation of bovine elastin mRNA due to alternative  
 RL splicing.";  
 RL Coll. Relat. Res. 7:235-247(1987).  
 DR EMBL; M19372; AAA30501.1; JOINED.  
 DR EMBL; M11422; AAA30501.1; JOINED.  
 DR EMBL; M19366; AAA30501.1; JOINED.  
 DR EMBL; M19367; AAA30501.1; JOINED.  
 DR EMBL; M19368; AAA30501.1; JOINED.  
 DR EMBL; M19369; AAA30501.1; JOINED.  
 DR EMBL; M19370; AAA30501.1; JOINED.  
 DR EMBL; M19371; AAA30501.1; JOINED.  
 DR EMBL; M22771; AAA30501.1; JOINED.  
 DR EMBL; M22772; AAA30501.1; JOINED.  
 DR EMBL; M22773; AAA30501.1; JOINED.  
 DR EMBL; M22774; AAA30501.1; JOINED.  
 DR EMBL; M22775; AAA30501.1; JOINED.  
 DR EMBL; M22988; AAA30501.1; JOINED.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOELASTIN.  
 FT NON TER 1  
 SQ SEQUENCE 666 AA; 56435 MW; BC5E62632BE1B71 CRC64;  
 Query Match 78.7%; Score 199; DB 2; Length 666;  
 Best Local Similarity 92.7%; Pred. No. 2.1e-08;  
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVPGFGA 41  
 Db 476 AAAGLPAGVPGVGLGVGVGPGVGLGVGAGVPGVPGFGA 516  
 RESULT 20  
 Q28098  
 ID Q28098 PRELIMINARY; PRT; 707 AA.  
 AC Q28098;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Elastin; NCBI gi: 163002 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85280426; PubMed=2992576;  
 RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,  
 RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;  
 RT "Structure of the 3' portion of the bovine elastin gene.";  
 RL Biochemistry 24:3075-3080(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88028442; PubMed=3665402;  
 RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,  
 RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;  
 RT "Sequence variation of bovine elastin mRNA due to alternative  
 RL splicing.";  
 RL Coll. Relat. Res. 7:235-247(1987).  
 DR EMBL; M19372; AAA30498.1; JOINED.  
 DR EMBL; M11422; AAA30498.1; JOINED.  
 DR EMBL; M19366; AAA30498.1; JOINED.  
 DR EMBL; M19367; AAA30498.1; JOINED.  
 DR EMBL; M19368; AAA30498.1; JOINED.  
 DR EMBL; M19369; AAA30498.1; JOINED.  
 DR EMBL; M19370; AAA30498.1; JOINED.  
 DR EMBL; M19371; AAA30498.1; JOINED.  
 DR EMBL; M22771; AAA30498.1; JOINED.  
 DR EMBL; M22772; AAA30498.1; JOINED.

DR EMBL; M22773; AAA30498.1; JOINED.  
 DR EMBL; M22774; AAA30498.1; JOINED.  
 DR EMBL; M22775; AAA30498.1; JOINED.  
 DR EMBL; M22988; AAA30498.1; JOINED.  
 DR EMBL; M23010; AAA30498.1; JOINED.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOELASTIN.  
 FT NON TER 1  
 SQ SEQUENCE 707 AA; 60346 MW; FDFD559BAB34CE33 CRC64;  
 Query Match 78.7%; Score 199; DB 2; Length 707;  
 Best Local Similarity 92.7%; Pred. No. 2.2e-08;  
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVPGFGA 41  
 Db 502 AAAGLPAGVPGVGLGVGVGPGVGLGVGAGVPGVPGFGA 542

RESULT 21  
 Q9ESZ9  
 ID Q9ESZ9 PRELIMINARY; PRT; 810 AA.  
 AC Q9ESZ9;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE ELN (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv;  
 RA Green E.D.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF289665; AAF99336.1; -.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOELASTIN.  
 FT NON TER 1  
 SQ SEQUENCE 810 AA; 67204 MW; 1ED61ED5AD4F40A2 CRC64;

Query Match 76.3%; Score 193; DB 2; Length 810;  
 Best Local Similarity 81.4%; Pred. No. 7.4e-08;  
 Matches 35; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVPGFGA 43  
 Db 558 AAAGLGAGVPGVPGAGAGVPGVPGFGAGAGVPGVPGFGA 600

RESULT 22  
 ELS\_MOUSE  
 ID ELS\_MOUSE STANDARD; PRT; 860 AA.  
 AC P54320;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Elastin precursor (Tropoelastin).  
 GN Name=Elm;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Lung;  
 RX MEDLINE=95130069; PubMed=7829060;  
 RA Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;

"Use of an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human chromosome 7.";

Genomics 23:125-131(1994).

-!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.

-!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.

-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.

-!- PTM: The crosslinks are made of deaminated lys.

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EMBL; U08210; AAA80155.1; -. PIR; A55210; EAMS. MGD; MG1:95317; Eln. InterPro; IPR003979; tropoelastin. PRINTS; PR01500; TROPOLASTIN. Connective tissue; Repeat; Signal; Structural protein. SIGNAL 1 27 Potential. CHAIN 28 860 Elastin. DISULFID 850 855 By similarity. SEQUENCE 860 AA; 71955 MW; 0C0B55AE1EDD7F1 CRC64;

Query Match 76.3%; Score 193; DB 1; Length 860;  
Best Local Similarity 81.4%; Pred. No. 7.7e-08;  
Matches 35; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY  
Db 1 AAAGLGAGIPLGVGVPGLVGCAGVPGVLGGVGAVPFGAGAGA 43  
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
608 AAAGLGAGVPGFAGAGVPGFAGAGVPGFAGAGVPGFAGAGA 650

RESULT 23 Q8C9L8 PRELIMINARY; PRT; 860 AA.  
AC AC Q8C9L8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DI 01-MAR-2004 (TrEMBLrel. 28, Last annotation update)  
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched DE library, clone:A630042119 product:elastin, full insert sequence (Elastin).  
GN Name=Eln.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RZ "High-efficiency full-length cDNA cloning.";  
RS Meth. Enzymol. 303:19-44(1999).  
RL Nature 409:685-690(2001).  
[2]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=92279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "Normaliza-tion and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[3]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=21085860; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=21085860; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=21085860; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
Nature 420:563-573(2002).  
[4]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu M., Hayashizaki Y.;  
Kanno H., Okazaki Y., Muramatsu M., Matsui S., Kawai J.,  
Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
ADACHI J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Kasukawa T., Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Nakamura M., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Onosato N., Okazaki Y., Saito R., Saichou H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sobabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
[7]  
SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.D., Fellings E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schafer C.F., Bhut N.K., Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Heise F., Diatchenko L., Marusic K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzyzinski M.I., Skalska U., Smallus D.E., Schnertzh A., Schein J.E., Jones S.J., Maier M.A.;  
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[8]  
SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RA Strausberg R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AK041860; BAC31084.1; -.  
DR EMBL; BC051649; AAH51649.1; -.  
DR MGD; MG1:95317; Eln.

GO: 0007519; P: myogenesis; IMP.  
GO: 0030833; P: regulation of actin filament polymerization; IMP.  
GO: 0043149; P: stress fiber formation; IMP.  
InterPro: IPR003979; Tropoelastin.  
PRINTS: PR01500; TROPOELASTIN.  
SEQUENCE 860 AA; 71938 MW; 7C340F2FFDC92E5 CRC64;  
Query Match 76.3%; Score 193; DB 2; Length 860;  
Best Local Similarity 81.4%; Pred. No. 7.7e-08;  
Matches 35; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 1 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGAGA 43  
Db 608 AAAGLGGVPGFGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGA 650  
RESULT 24  
ELD\_BOVIN  
ID ELS BOVIN STANDARD; PRT; 747 AA.  
AC P04985; P04986; P04987; Q29421;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Elastin precursor (Tropoelastin).  
GN Name=ELN;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
ON NCBI\_TaxID=9913;  
OX [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87194772; PubMed=3032943;  
RA Raju K., Anwar R.A.;  
RT "Primary structures of bovine elastin a, b, and c deduced from the  
sequences of cDNA clones."  
RL J. Biol. Chem. 262:5755-5762 (1987).  
RN [2]  
RP SEQUENCE OF 1-27 FROM N.A.  
RX TISSUE=Nuchal ligament;  
RC MEDLINE=89274159; PubMed=2543440;  
RA Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,  
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,  
RA Rosenbloom J.;  
RT "Structure of the bovine elastin gene and S1 nuclease analysis of  
alternative splicing of elastin mRNA in the bovine nuchal ligament";  
RL Biochemistry 28:2365-2370 (1989).  
RN [3]  
RP SEQUENCE OF 1-27 FROM N.A.  
RX MEDLINE=91234332; PubMed=2031719;  
RA Manohar A., Shi W., Anwar R.A.;  
RT "Partial characterization of bovine elastin gene; comparison with the  
gene for human elastin";  
RL Biochem. Cell Biol. 69:185-192 (1991).  
RN [4]  
RP DISULFIDE BOND.  
RX MEDLINE=92337651; PubMed=1632791;  
RA Brown P.L., Mecham R., Tisdale C., Mecham R.P.;  
RT "The cysteine residues in the carboxy terminal domain of tropoelastin  
form an intrachain disulfide bond that stabilizes a loop structure and  
positively charged pocket";  
RL Biochem. Biophys. Res. Commun. 186:549-555 (1992).  
RN [5]  
RP FUNCTION: Major structural protein of tissues such as aorta and  
nuchal ligament, which must expand rapidly and recover completely.  
RN [6]  
RP SUBUNIT: The polymeric elastin chains are cross-linked together  
into an extensible 3D network.  
RN [7]  
RP SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.  
RN [8]  
RP ALTERNATIVE PRODUCTS:  
RN [9]  
RP Event=Alternative splicing; Named isoforms=3;  
CC Name=1; Synonyms=A;  
CC IsoId=P04985-1; Sequence=Displayed;  
CC Name=2; Synonyms=B;  
CC IsoId=P04985-2; Sequence=VSP\_004239;  
CC

GO: 0007519; P: myogenesis; IMP.  
GO: 0030833; P: regulation of actin filament polymerization; IMP.  
GO: 0043149; P: stress fiber formation; IMP.  
InterPro: IPR003979; Tropoelastin.  
PRINTS: PR01500; TROPOELASTIN.  
SEQUENCE 860 AA; 71938 MW; 7C340F2FFDC92E5 CRC64;  
Query Match 76.3%; Score 193; DB 2; Length 860;  
Best Local Similarity 81.4%; Pred. No. 7.7e-08;  
Matches 35; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 1 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPLGVGAGVPGFGAG 43  
Db 608 AAAGLGGVPGFGAGAGVPGFGAGAGVPGFGAGVPGFGAG 650  
RESULT 24  
ELD\_BOVIN  
ID ELS BOVIN STANDARD; PRT; 747 AA.  
AC P04985; P04986; P04987; Q29421;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Elastin precursor (Tropoelastin).  
GN Name=ELN;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
ON NCBI\_TaxID=9913;  
OX [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87194772; PubMed=3032943;  
RA Raju K., Anwar R.A.;  
RT "Primary structures of bovine elastin a, b, and c deduced from the  
sequences of cDNA clones."  
RL J. Biol. Chem. 262:5755-5762 (1987).  
RN [2]  
RP SEQUENCE OF 1-27 FROM N.A.  
RX TISSUE=Nuchal ligament;  
RC MEDLINE=89274159; PubMed=2543440;  
RA Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,  
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,  
RA Rosenbloom J.;  
RT "Structure of the bovine elastin gene and S1 nuclease analysis of  
alternative splicing of elastin mRNA in the bovine nuchal ligament";  
RL Biochemistry 28:2365-2370 (1989).  
RN [3]  
RP SEQUENCE OF 1-27 FROM N.A.  
RX MEDLINE=91234332; PubMed=2031719;  
RA Manohar A., Shi W., Anwar R.A.;  
RT "Partial characterization of bovine elastin gene; comparison with the  
gene for human elastin";  
RL Biochem. Cell Biol. 69:185-192 (1991).  
RN [4]  
RP DISULFIDE BOND.  
RX MEDLINE=92337651; PubMed=1632791;  
RA Brown P.L., Mecham R., Tisdale C., Mecham R.P.;  
RT "The cysteine residues in the carboxy terminal domain of tropoelastin  
form an intrachain disulfide bond that stabilizes a loop structure and  
positively charged pocket";  
RL Biochem. Biophys. Res. Commun. 186:549-555 (1992).  
RN [5]  
RP FUNCTION: Major structural protein of tissues such as aorta and  
nuchal ligament, which must expand rapidly and recover completely.  
RN [6]  
RP SUBUNIT: The polymeric elastin chains are cross-linked together  
into an extensible 3D network.  
RN [7]  
RP SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.  
RN [8]  
RP ALTERNATIVE PRODUCTS:  
RN [9]  
RP Event=Alternative splicing; Named isoforms=3;  
CC Name=1; Synonyms=A;  
CC IsoId=P04985-1; Sequence=Displayed;  
CC Name=2; Synonyms=B;  
CC IsoId=P04985-2; Sequence=VSP\_004239;  
CC

[illegible]

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AC P07916;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (tropoelastin) (Fragment).
GN Name=ELN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87242320; PubMed=3593675;
RA Bressan G.M., Argos P., Stanley K.K.;
RT "Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning.";
RL Biochemistry 26:1497-1503(1987).
RN [2]
RP SEQUENCE OF 85-750 FROM N.A. (ISOFORM 2).
RX MEDLINE=88309083; PubMed=2841924;
RA Baule V.J., Foster J.A.;
RT "Multiple chick tropoelastin mRNAs.";
RL Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
RN [3]
RP SEQUENCE OF 457-750 FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=87297534; PubMed=3502711;
RA Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
RT "Sequence analysis of elastin cDNA from chick aorta and tissue-
RT specific transcription of the elastin gene in developing chick
RT embryo.";
RL Arch. Biochem. Biophys. 256:455-461(1987).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P07916-1; Sequence=Displayed;
CC Name=2; Synonyms=Embryonic;
CC IsoId=P07916-2; Sequence=VSP_004241, VSP_004242;
CC -!- PTM: The crosslinks are made of deaminated Lys.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M18633; AAA48761.1; -
DR EMBL; M21880; AAA49082.1; -
DR EMBL; M15889; AAA49108.1; -
DR PIR; A26601; A26601.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR003979; Tropoelastin.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR01500; TROPELASTIN
KW Alternative splicing; Connective tissue; Repeat; Signal;
KW Structural protein.
FT NON_TER 1 1
FT SIGNAL <1 24
FT CHAIN 25 750 Elastin.
FT DOMAIN 83 686 8 X tandem repeats.
FT REPEAT 83 127 1.
FT REPEAT 219 262 2.

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FT REPEAT 263 318
FT REPEAT 319 393
FT REPEAT 394 482
FT REPEAT 483 554
FT REPEAT 555 619
FT REPEAT 620 686
FT DISULFID 739 745
FT MOD_RES 63 63
FT MOD_RES 66 66
FT MOD_RES 111 111
FT MOD_RES 115 115
FT MOD_RES 156 156
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FT
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FT CONFLICT 536 536
FT CONFLICT 571 571
FT CONFLICT 610 610
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FT CONFLICT 667 667
SQ SEQUENCE 750 AA; 63697 MW; E57ECD60C6E8556F CRC64;

Query Match 50.0%; Score 126.5; DB 1; Length 750;
Best Local Similarity 68.3%; Pred. No. 0.014;
Matches 28; Conservative 4; Mismatches 6; Indels 3; Gaps 3;

OY 6 GAGIPGLGV-GVGPGLGV-GAGVPGLV-GAGVPGFGAGA 43
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DB 466 GVGPGVGPGVGPGVGPGVGPGVGPGVGPGVGPGVG 506
| | | | | | | | | | | | | | | | | | | | | |

RESULT 28
Q26675 PRELIMINARY; PRT; 907 AA.
AC Q26675
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sporozoite surface antigen.
GN Name=spag-1;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Hissar;
RX MEDLINE=92365719; PubMed=1501630;
RA Hall R., Hunt P.D., Carrington M., Simmons D.L., Williamson S.,
RA Tait A.;
RT "Mimicry of elastin repetitive motifs by Theileria annulata sporozoite
RT surface antigen.";
RL Mol. Biochem. Parasitol. 53:105-112(1992).
DR EMBL; M63017; AAA30134.1; -.
DR PIR; A33934; A33934.
DR PIR; A45560.
DR InterPro; IPR000600; ROK.
DR InterPro; IPR008845; Sporozoite_P67.
DR Pfam; PF05642; Sporozoite_P67; I.
DR PROSITE; PS01125; ROK; UNKNOWN_1.
SQ SEQUENCE 907 AA; 91885 MW; 589CE55C740D4835 CRC64;

Query Match 49.6%; Score 125.5; DB 2; Length 907;
Best Local Similarity 50.9%; Pred. No. 0.02; Indels 15; Gaps 3;
Matches 29; Conservative 4; Mismatches 9;

QY 6 GAGIPGLGV-GVGVPGLGV-GAGVPGLGV-----GAGVPGFAGADEGV 47
Db 180 GVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVG 236

RESULT 29
Q8PZF2 PRELIMINARY; PRT; 196 AA.
AC Q8PZF2; 2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein MM0542.
GN OrderedLocusNames=MM0542;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wieser A., Baumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013279; AA030238.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0007049; P:cell cycle; IEA.
DR InterPro; IPR00158; FtsZ.
DR InterPro; IPR001451; Hexapep_transf.
DR PRINTS; PR00423; CELLDIVISF7S.
DR PROSITE; PS00101; HEXAPEP_TRANSFERSASES; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 196 AA; 15462 MW; BB808A7BAC7D028B CRC64;

Query Match 46.2%; Score 117; DB 2; Length 196;
Best Local Similarity 57.1%; Pred. No. 0.03; Indels 8; Gaps 4;
Matches 28; Conservative 8; Mismatches 5;

QY 4 GLGAGIPGLGVGVPGVGLGVGAGVPGVGLGVGAGV-----PGFGAGADEGV 47
Db 34 GVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVG 79

RESULT 30
Q6ZUN2
ID Q6ZUN2 PRELIMINARY; PRT; 559 AA.
AC Q6ZUN2;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43523.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK125511; BAC86188.1; -.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR SQ SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 45.5%; Score 115; DB 2; Length 559;
Best Local Similarity 63.6%; Pred. No. 0.095; Indels 6; Gaps 3;
Matches 28; Conservative 2; Mismatches 8;

QY 1 AAAGLGAGIPGLGV-GVGVPGLGV-GAGVPGLGV---GAGVPG 38
Db 313 AAAGLVPGGPGFGVGVGVGVGVGVGVGVGVGVGVGVGVGVG 356

Search completed: November 19, 2004, 16:36:50
Job time : 11.907 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 34.9467 Seconds  
(without alignments)  
1755.321 Million cell updates/sec

Title: US-09-743-818a-73

Perfect score: 872

Sequence: 1 GVRSLSPLELREGDPSSOH.....LSPFPGACLGKACGRKRK 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	872	100.0	171	3	AAV69137
2	872	100.0	200	2	AAV01305
3	872	100.0	216	2	AAV01310
4	872	100.0	731	3	AAV69068
5	872	100.0	731	4	AAV66657
6	872	100.0	731	6	ABU08725
7	872	100.0	731	7	ADL96420
8	872	100.0	733	2	AAV56653
9	872	100.0	733	2	AAV01301
10	872	100.0	733	2	AAV01301
11	872	100.0	757	7	ABG75223
12	855.5	98.1	730	2	AAW46315
13	725	83.1	183	2	AAV01311
14	725	83.1	183	3	AAV69138
15	725	83.1	692	7	AAE40134
16	725	83.1	698	2	AAV01302
17	725	83.1	698	3	AAV69069
18	725	83.1	730	5	AAO17360
19	725	83.1	730	8	ADQ13747
20	723	82.9	147	2	AAV01304
21	717	82.2	663	7	ADM03792
22	710.5	81.5	660	2	AAV01303
23	612	70.2	617	7	ADB64761
24	612	70.2	712	3	AAV08630
25	612	70.2	730	3	AAV08631

26	609	69.8	711	7	ADB40132
27	482	55.3	864	7	ADE56670
28	475	54.5	870	7	ADE08527
29	318	36.5	60	2	AAV01306
30	280	32.1	472	1	AAV88422
31	274	31.4	294	1	AAV82484
32	269.5	30.9	515	3	AAV69135
33	269.5	30.9	571	3	AAV69071
34	253	29.0	47	2	AAV01307
35	212.5	24.4	199	6	AAV66661
36	212.5	24.4	199	6	ABU08735
37	212.5	24.4	199	7	ADL96424
38	212.5	24.4	200	4	AAV66658
39	212.5	24.4	200	6	ABU08726
40	212.5	24.4	200	7	ADL96421
41	212	24.3	201	2	AAW46316
42	206.5	23.7	366	8	ADP31574
43	206.5	23.7	384	8	ADP31575
44	206.5	23.7	906	8	ADP31573
45	204	23.4	738	2	AAV56163
46	201.5	23.1	279	8	ADP31572
47	200	22.9	681	4	AAV82610
48	199.5	22.9	691	4	AAV82609
49	199.5	22.9	291	4	AAV82608
50	199	22.8	528	4	AAV82611
51	198.5	22.8	252	8	ADP31571
52	197	22.6	951	8	ADP31413
53	195.5	22.4	235	2	AAW05704
54	195.5	22.4	235	2	AAV79126
55	195.5	22.4	261	2	AAV79137
56	195.5	22.4	534	8	ADP31164
57	195.5	22.4	537	8	ADP31162
58	195.5	22.4	641	2	AAV28843
59	195.5	22.4	641	3	AAV95856
60	195.5	22.4	641	4	AAV62332
61	195.5	22.4	641	6	ABP72663
62	195.5	22.4	641	6	AAV4812
63	195.5	22.4	641	6	AAV4812
64	195.5	22.4	641	7	ADK65581
65	195.5	22.4	641	8	ADJ57052
66	195.5	22.4	641	8	ADP12515
67	195	22.4	1002	6	AAE36885
68	194.5	22.3	651	2	AAV40097
69	194.5	22.3	651	5	AAU11781
70	194.5	22.3	718	2	AAV53346
71	194.5	22.3	718	3	AAV59070
72	194	22.2	646	2	AAW27178
73	194	22.2	646	7	ADB61321
74	194	22.2	646	7	ADC35240
75	194	22.2	646	7	ADM46149
76	194	22.2	651	6	AAE36884
77	193.5	22.2	294	7	ADC35283
78	193	22.1	691	6	AAE36887
79	191	21.9	648	6	AAE36869
80	190.5	21.8	762	8	ADP31012
81	190.5	21.8	885	8	ADP31011
82	189	21.7	271	2	AAV50044
83	189	21.7	447	6	AAE36868
84	189	21.7	606	2	AAV99053
85	189	21.7	606	2	AAV40100
86	189	21.7	630	5	AAV50042
87	189	21.7	676	5	AAV50047
88	189	21.7	989	5	AAV50038
89	189	21.7	1255	5	AAV50037
90	189	21.7	1880	5	AAV50039
91	188.5	21.6	889	8	ADP31648
92	187.5	21.5	718	2	AAV4308
93	185	21.2	291	2	AAV49738
94	184	21.1	479	2	AAV49739
95	183.5	21.0	287	2	AAV49737
96	182.5	20.9	364	5	AAV50043
97	182.5	20.9	604	2	AAV99057
98	182.5	20.9	773	5	AAV50045

Ade40132 Human NOV  
Ade56670 Rat Prote  
Ade08527 Novel pro  
Aay01306 Human tro  
Aab88422 Human mem  
Aap82484 Tropoelas  
Aay69135 Amino aci  
Aay69071 Amino aci  
Aay01307 Human tro  
Aab66661 MFU-5.4/  
Abu08735 Human ela  
Adl96424 Human ela  
Aab66658 MFU-2.4/  
Abu08726 Human ela  
Adl96421 Human ela  
Aaw46316 Non-natur  
Adp31574 Human sec  
Adp31575 Human sec  
Adp31573 Human sec  
Aaw56163 New DNA s  
Adp31572 Human sec  
Aab82609 Spider re  
Aab82610 Spider re  
Aab82608 Spider re  
Aab82611 Spider re  
Adp31571 Human sec  
Adp31413 Human sec  
Aaw05704 Glyciner  
Aaw79136 Epstein B  
Aaw79137 FLGA Gly-  
Adp31164 Human sec  
Adp31162 Human sec  
Adp31163 Human sec  
Aay28843 Epstein B  
Aay95856 Epstein B  
Aab62332 EBV tethe  
Abp72663 Epstein-B  
Aae34812 Epstein-B  
Adk65581 Human her  
Adj57052 Epstein-B  
Adp12515 Protein e  
Aae36885 Argiope t  
Aay40097 Spider si  
Aau11781 Spider na  
Aaw53346 Nephila c  
Aaw59070 N. clavi  
Aaw27178 Nephila c  
Adb61321 Spider si  
Adc35240 Maspi sil  
Adm46149 Nephila c  
Aae36884 Argiope t  
Adc35283 ADP-2 sil  
Aae36887 Dolomedes  
Aae36869 Argiope t  
Adp31012 Human sec  
Adp31011 Human sec  
Aam50044 N. clavi  
Aae36868 Argiope a  
Aar99053 Spider dr  
Aay40100 Polymer o  
Aam50047 N. clavi  
Aam50042 N. clavi  
Aam50038 N. clavi  
Aam50037 N. clavi  
Aam50039 N. clavi  
Adp31648 Human sec  
Aar14308 N.clavi  
Aaw49738 Protein p  
Aaw49739 Protein p  
Aaw49737 Protein p  
Aam50043 N. clavi  
Aar99057 Spider dr  
Aam50045 N. clavi

99	182.5	20.9	777	5	AAM50046	Aam50046 N. clavip
100	182	20.9	281	2	AAM49736	Aaw49736 Protein p

## ALIGNMENTS

RESULT 1	
AA069137	AA069137 standard; protein; 171 AA.
ID	AA069137
XX	XX
AC	AA069137;
XX	XX
DT	30-MAY-2000 (first entry)
XX	XX
DE	Amino acid sequence of a human tropoelastin derivative.
XX	XX
KW	Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
KW	hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
KW	peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
XX	XX
OS	Homo sapiens.
XX	XX
BN	WO200004043-A1.
XX	XX
PD	27-JAN-2000.
XX	XX
PF	19-JUL-1999; 99WO-AU000580.
XX	XX
PR	17-JUL-1998; 98AU-00004723.
XX	XX
PA	(UNSY ) UNIV SYDNEY.
XX	XX
PI	Weiss AS;
XX	XX
DR	WPI; 2000-182399/16.
XX	XX
PT	New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.

Disclosure; Page 133-134; 136pp; English.

The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

[illegible]

61 IQGVVVGAPAAAAAAXAAQFGLVGAAGLGLGVGGLGVFGVGLGIPAAAAAK 120  
QY

61 IQGVVVGAPAAAAAAXAAQFGLVGAAGLGLGVGGLGVFGVGLGIPAAAAAK 120  
Db

121 AAKYGAAGLGVVLGGAGQFPLGGVAARPCFGLSPIPPGCACILGKACGRKK 171  
QY

121 AAKYGAAGLGVVLGGAGQFPLGGVAARPCFGLSPIPPGCACILGKACGRKK 171  
Db

## RESULT 2

AAV01305			
ID	AAV01305 standard; protein; 200 AA.		
XX			
XX	AAV01305;		
XX			
XX	07-JUN-1999 (first entry)		
DT			
XX			
XX	Human tropoelastin derivative SHELgamma.		
DE			
DE			
XX			
XX	Tropoelastin; nTE; elastin; glycosaminoglycan; GAG-binding; medical;		
KW	pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;		
KW	hand lotion; surgical implant; industrial product; human; SHEL; variant.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PN	WO9903886-A1.		
XX			
PD	28-JAN-1999.		
XX			
PF	17-JUL-1998; 98WO-AU000564.		
XX			
PR	18-JUL-1997; 97AU-00008117.		
XX			
PA	(UNSY ) UNIV SYDNEY.		
XX			
PI	Weiss AS;		
XX			
DR	WPI; 1999-132162/11.		
DB	N-PSNR. AAV27707.		

XX New derivatives of human tropoelastin - with elastin-like or  
PT macromolecular binding properties, useful e.g. as surgical implants.  
PT  
XX  
XX  
PS Claim 15; Fig 8; 82pp; English.  
XX  
XX The invention relates to a derivative or variant of human tropoelastin  
CC (htrf) having elastin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives  
CC or hybrid proteins containing the derivatives are useful in medical,  
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26a, from htrf. The present sequence represents a human  
CC tropoelastin derivative SHBLgamma

```

XX
SQ Sequence 200 AA;
Query Match 100.0%; Score 872; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 5.2e-58;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Qy	1	GVRSLSP	PELR	REGD	PSS	SOHL	P	STP	SP	PRV	PCAL	AAAA	AAK	YCA	AV	PG	V	GL	GL	GL	GG	VG	60
Db	30	GVRSLSP	ELR	REGD	PSS	SOHL	P	STP	SP	PRV	PCAL	AAAA	AAK	YCA	AV	PG	V	GL	GL	GL	GG	VG	89
Qy	61	IPGV	VY	GAG	P	AAAA	AAAA	AAAA	AAK	AAQ	FL	VG	AG	L	GL	GL	GL	GV	PG	VG	GL	G	120
Db	90	IPGV	VY	GAG	P	AAAA	AAAA	AAAA	AAK	AAQ	FL	VG	AG	L	GL	GL	GL	GV	PG	VG	GL	G	149

166 AAKYGAAGLGGVLGGAGQFPLGGVAARPFGFLSPFPFGGACLGKACGRKPK 216

QY  
61 IPGGTVGAGPAAAAAAAAAQAQFGLVGAAGLGLGVGGLGVPGVGGGGIPPPAAAAAK 120

Db	621	IPGVVVGAGPAAAAAATAAATAAQAQGLVGAAGLGLGVGGVGLGVPVGGVGLGIPAAAAK	680
QY	121	AAKYGAAGLGGVGLGAGQPLGVAAPGFGLSPIPPGGACLGKACGRKK	171
Db	681	AAKYGAAGLGGVGLGAGQPLGVAAPGFGLSPIPPGGACLGKACGRKK	731
RESULT 5			
AAAB66657	ID	AAAB66657 standard; protein; 731 AA.	
XX	AC	AAAB66657;	
XX	AC		
XX	DT	05-APR-2001 (first entry)	
XX	DE	Human elastin protein without signal peptide.	
XX	KW	Minimal function unit; MFU; human; elastin prosthetic.	
XX	OS	Homo sapiens.	
XX	XX	WO200100666-A2.	
XX	XX		
XX	PD	04-JAN-2001.	
XX	XX		
XX	PF	29-JUN-2000; 2000WO-US017829.	
XX	XX		
XX	PR	29-JUN-1999; 99US-00340736.	
XX	XX		
XX	PA	(PROT-) PROTEIN SPECIALTIES LTD.	
XX	PA	(HSCR-) HSC RES & DEV LP.	
XX	PI	Rothstein A, Keeley F, Rothstein S, Stahl R;	
XX	XX	WPI; 2001-102886/11.	
XX	XX		
XX	PT	Novel polypeptides that comprise three beta-sheet/beta-turn structures	
XX	PT	and are not naturally occurring fibrous protein, used to produce	
XX	PT	prostheses suitable for implantation into humans, and cosmetic materials.	
XX	XX		
XX	PS	Claim 1; Fig 1; 39pp; English.	
XX	XX		
XX	CC	The present invention relates to a minimal functional unit (MFU) of human	
XX	CC	elastin polypeptide. This protein is useful in a cosmetic material or a	
XX	CC	prosthetic material such as prosthesis for blood vessel replacements, for	
XX	CC	heart valve replacement, tissue replacement, for covering burns, for	
XX	CC	covering wounds and stents	
XX	SQ	Sequence 731 AA;	
Query Match			
Best Local Similarity 100.0%; Score 872; DB 4; Length 731;			
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GVRSLSPDLREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGVG	60
Db	561	GVRSLSPDLREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGVG	620
QY	61	IPGVVVGAGPAAAAAATAAATAAQAQGLVGAAGLGLGVGGVGLGIPAAAAK	120
Db	621	IPGVVVGAGPAAAAAATAAATAAQAQGLVGAAGLGLGVGGVGLGIPAAAAK	680
QY	121	AAKYGAAGLGGVGLGAGQPLGVAAPGFGLSPIPPGGACLGKACGRKK	171
Db	681	AAKYGAAGLGGVGLGAGQPLGVAAPGFGLSPIPPGGACLGKACGRKK	731
RESULT 6			
ABU08725	ID	ABU08725 standard; protein; 731 AA.	
XX	XX		
XX	AC	ABU08725;	

Db 561 GVRRLSPLELREGDPSSQHLPTSPSPRPVPGALAAAKAAKYGAAPVGLGALGVG 620  
 QY 61 IPGVVVGAGPAAAAAATAAKAQAQFGLVGAAGLGLGVGLGVGVGGVGGIPPPAAAAK 120  
 Db 621 IPGVVVGAGPAAAAAATAAKAQAQFGLVGAAGLGLGVGLGVGGVGGVGGIPPPAAAAK 680  
 QY 121 AAKYGAAGLGVGGAGQFPLGGVAAAPGFGLSPIFFGGACLGKACGRKK 171  
 Db 681 AAKYGAAGLGVGGAGQFPLGGVAAAPGFGLSPIFFGGACLGKACGRKK 731

## RESULT 7

ADL96420  
 ID ADL96420 standard; protein; 731 AA.

AC ADL96420;  
 XX  
 XX 20-MAY-2004 (first entry)  
 XX  
 DE Human elastin protein fragment.  
 XX  
 KW fibrous protein; prosthesis; elastin; lamprin; spider silk protein;  
 KW blood vessel; wound; burn healing; collagen.  
 XX  
 OS Homo sapiens.

XX  
 FH Key  
 FT Region 19..160  
 FT Region /note= "region specifically claimed in claim 6"  
 FT Region 188..367  
 FT Region /note= "region specifically claimed in claim 6"  
 FT Region 374..499  
 FT Region /note= "region specifically claimed in claim 6"  
 FT Region 607..717  
 FT Region /note= "region specifically claimed in claim 6"  
 XX  
 US2003166846-A1.

XX  
 PD 04-SEP-2003.

XX  
 PF 28-SEP-2001; 2001US-00964662.

PR 07-AUG-1996; 96US-0023522P.

PR 07-AUG-1997; 97US-00911364.

PR 29-JUN-1999; 99US-00340736.

XX (ROTH/) ROTHSTEIN A.  
 PA (KEEL/) KELEY F.  
 PA (ROTH/) ROTHSTEIN S.

XX  
 PI Rothstein A, Keeley F, Rothstein S;  
 DR WPI; 2003-898105/82.

XX  
 XX  
 XX

PT Polypeptide for constructing human elastin-like prostheses such as tubes  
 FT for blood vessel replacement and sheets for other uses such as wound or  
 FT burn healing, comprises three beta sheets and three beta turns.

XX  
 PS Claim 5; Fig 1B; 17pp; English.

XX  
 CC This invention describes a polypeptide that comprises three beta  
 CC sheet/beta turn structures and that is not a naturally occurring fibrous  
 CC protein. The invention also describes a prosthesis comprising an animal,  
 CC metal or synthetic material, where the surface is coated with the  
 CC polypeptide, a cosmetic material comprising the polypeptide, an elastic  
 CC material comprising the polypeptide, a high tensile strength material  
 CC comprising the polypeptide, a material comprising two or more  
 CC polypeptides selected from (a) a polypeptide consisting essentially of a  
 CC portion of the polypeptide comprising at least three beta sheet/beta turn  
 CC structures, (b) a polypeptide consisting essentially of a portion of the  
 CC amino acid sequence of an animal elastin comprising at least three beta  
 CC sheets/beta turns, (c) a polypeptide consisting essentially of a portion

CC of lamprin comprising at least three beta sheets/beta turns, and (d) a  
 CC polypeptide consisting essentially of a spider silk protein comprising at  
 CC least three beta sheets/beta turns, a polypeptide having the primary  
 CC structure of a portion of a naturally occurring fibrous protein and a  
 CC secondary structure comprising at least three beta sheets/beta turns,  
 CC where each of the beta sheet/beta turn structures comprises from 3 to  
 CC about 7 amino acids and the polypeptide is not a naturally occurring  
 CC fibrous protein. The minimal functional unit (MFU) of the invention is  
 CC useful to construct human elastin-like prostheses such as tubes for blood  
 CC vessel replacement and sheets for other uses such as wound or burn  
 CC healing. Alternatively the MFU can be co-aggregated with other proteins,  
 CC for example collagen, to provide prosthesis material that resembles the  
 CC natural structural materials of the body. The MFU based material is  
 CC subject to infiltration of cells growing in the patient, including  
 CC endothelial cells, and the prosthesis can become a permanent living  
 CC tissue replacement. The material is more biocompatible than other elastin  
 CC -containing materials proposed for prostheses.  
 XX  
 SQ Sequence 731 AA;

Query Match 100.0%; Score 872; DB 7; Length 731;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-57;  
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVRRLSPLELREGDPSSQHLPTSPSPRPVPGALAAAKAAKYGAAPVGLGALGVG 60  
 Db 561 GVRRLSPLELREGDPSSQHLPTSPSPRPVPGALAAAKAAKYGAAPVGLGALGVG 620  
 QY 61 IPGVVVGAGPAAAAAATAAKAQAQFGLVGAAGLGLGVGLGVGVGGVGGIPPPAAAAK 120  
 Db 621 IPGVVVGAGPAAAAAATAAKAQAQFGLVGAAGLGLGVGLGVGGVGGVGGIPPPAAAAK 680  
 QY 121 AAKYGAAGLGVGGAGQFPLGGVAAAPGFGLSPIFFGGACLGKACGRKK 171  
 Db 681 AAKYGAAGLGVGGAGQFPLGGVAAAPGFGLSPIFFGGACLGKACGRKK 731

## RESULT 8

AAR56653

ID AAR56653 standard; protein; 733 AA.

XX  
 AC AAR56653;

DT 25-MAR-2003 (revised)  
 DT 22-MAR-1995 (first entry)

XX  
 XX Synthetic human tropoelastin (SHEL).

DE Tropoelastin; pharmaceutical; surgical dressing.

XX  
 KW Synthetic.

OS  
 XX WO9414958-A1.

XX  
 PN 07-JUL-1994.

PD  
 XX 16-DEC-1993; 93WO-AU000655.

PF  
 XX 22-DEC-1992; 92AU-00006520.

PR  
 XX 28-JUN-1993; 93AU-00009661.

XX  
 PA (UNSY ) UNIV SYDNEY.

XX  
 PI Weiss AS, Martin SL;

XX  
 XX WPI; 1994-263633/32.

XX  
 XX N-PSDB; AAQ70941.

XX  
 XX Synthetic polynucleotide(s) - encode recombinant tropoelastins and  
 XX variants.

XX  
 XX Disclosure; Page 30; 77pp; English.

XX  
 XX

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us-09-743-818a-73.rag

CC Human synthetic tropoelastin is susceptible to hydrolytic breakdown of  
CC the crosslinks. Such material may be useful in e.g. surgical  
CC applications, where the gradual loss of material over time is intended.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 733 AA;  
Query Match 100.0%; Score 872; DB 2; Length 733;  
Best Local Similarity 100.0%; Pred. No. 1.8e-57;  
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GVRSLSPELREGDPSSQHLPTSPSPRVPGLAALAAKAAKYAAVPGVGLGALGGVG 60  
Db 563 GVRSLSPELREGDPSSQHLPTSPSPRVPGLAALAAKAAKYAAVPGVGLGALGGVG 622  
QY 61 IPGVVVGAGPAAAAAATAAQAQGLVGAAGLGLGVGGVPGVGGVGGVGGVGGVGGV 120  
Db 623 IPGVVVGAGPAAAAAATAAQAQGLVGAAGLGLGVGGVPGVGGVGGVGGVGGVGGV 682  
QY 121 AAKYGAAGLGGVGLGAGQPLGGVAARPGFGLSPIPPGGACLGKACGRKK 171  
Db 683 AAKYGAAGLGGVGLGAGQPLGGVAARPGFGLSPIPPGGACLGKACGRKK 733  
RESULT 9  
AAV01301  
ID AAV01301 standard; protein; 733 AA.  
AC AAV01301;  
XX  
XX 07-JUN-1999 (first entry)  
DT  
DE Amino acid sequence of synthetic human tropoelastin SHEL.  
XX  
KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX WO9903886-A1.  
XX  
XX 28-JAN-1999.  
PD  
PF 17-JUL-1998; 98WO-AU000564.  
XX  
PR 18-JUL-1997; 97AU-00008117.  
XX  
PA (UNSY ) UNIV SYDNEY.  
XX  
PI Weiss AS;  
XX  
DR WPI; 1999-132162/11.  
DR N-PSDB; AAX27704.  
XX  
PT New derivatives of human tropoelastin - with elastin-like or  
PT macromolecular binding properties, useful e.g. as surgical implants.  
XX  
PS Disclosure; Fig 1; 82pp; English.  
XX  
CC The invention relates to a derivative or variant of human tropoelastin  
CC (hTE) having elastin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives  
CC or hybrid proteins containing the derivatives are useful in medical,  
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26A, from hTE. The present sequence represents the amino acid  
CC sequence of the synthetic human tropoelastin SHEL

XX  
SQ Sequence 733 AA;  
Query Match 100.0%; Score 872; DB 2; Length 733;  
Best Local Similarity 100.0%; Pred. No. 1.8e-57;  
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GVRSLSPELREGDPSSQHLPTSPSPRVPGLAALAAKAAKYAAVPGVGLGALGGVG 60  
Db 563 GVRSLSPELREGDPSSQHLPTSPSPRVPGLAALAAKAAKYAAVPGVGLGALGGVG 622  
QY 61 IPGVVVGAGPAAAAAATAAQAQGLVGAAGLGLGVGGVPGVGGVGGVGGVGGVGGV 120  
Db 623 IPGVVVGAGPAAAAAATAAQAQGLVGAAGLGLGVGGVPGVGGVGGVGGVGGVGGV 682  
QY 121 AAKYGAAGLGGVGLGAGQPLGGVAARPGFGLSPIPPGGACLGKACGRKK 171  
Db 683 AAKYGAAGLGGVGLGAGQPLGGVAARPGFGLSPIPPGGACLGKACGRKK 733  
RESULT 10  
ABG75223  
ID ABG75223 standard; protein; 757 AA.  
XX  
XX ABG75223;  
AC  
XX 12-FEB-2004 (first entry)  
DT  
DE Human tropoelastin protein.  
XX  
KW Human; tropoelastin; elastin; body vessel occlusion; stenosis;  
KW vascular smooth muscle cell; elastin signaling; vasotropic.  
XX  
OS Homo sapiens.  
XX WO2003082203-A2.  
XX  
XX 09-OCT-2003.  
XX  
XX 27-MAR-2003; 2003WO-US009391.  
XX  
XX 27-MAR-2002; 2002US-0368084P.  
XX  
XX (UTAH ) UNIV UTAH RES FOUND.  
XX  
XX Li DY, Karnik S;  
XX WPI; 2003-833516/77.  
XX  
XX Use of an agent that promotes elastin signaling in smooth muscle cells  
XX for e.g. decreasing or preventing occlusion of a body vessel by smooth  
XX muscle cells, treating or preventing obstructive vascular disease, or  
XX preventing stenosis.  
XX  
XX Claim 24; Page 138-141; Opp; English.  
XX  
XX The present invention relates to the use of an agent that promotes  
XX elastin signaling in smooth muscle cells for decreasing or preventing  
XX occlusion of a body vessel by smooth muscle cells, decreasing vascular  
XX obstruction, promoting actin stress fiber formation or actin  
XX polymerisation, increasing F:G actin ratio in a smooth muscle cell,  
XX treating or preventing obstructive vascular disease (e.g. restenosis), or  
XX preventing stenosis. The agent that promotes elastin signaling in smooth  
XX muscle cells is useful for decreasing or preventing occlusion of a body  
XX vessel by smooth muscle cells, decreasing vascular obstruction, promoting  
XX actin stress fiber formation or actin polymerization, increasing F:G  
XX actin ratio in a smooth muscle cell, treating or preventing obstructive  
XX vascular disease (e.g. restenosis following angioplasty), or preventing  
XX stenosis. It is also useful in manufacturing a medicament for the  
XX treatment or prevention of occlusion of a vessel. The present sequence is  
XX the human tropoelastin protein as shown in the exemplification of the  
XX invention

Claim 5; Fig 1B; 39pp; English.

XX This represents the human elastin sequence containing the minimal  
 CC functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a  
 CC polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is  
 CC not a naturally occurring fibrous protein. Each beta-sheet structure has  
 CC 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at  
 CC least 1 amino acid that can take part in crosslinking. The polypeptide  
 CC can also be derived from the sequences of animal elastin, lamprin and  
 CC spider silk protein. The MFU polypeptides are self-aligning peptides  
 CC having the same primary structure as part of a natural fibrous protein.  
 CC They are used to coat prostheses made of animal or synthetic material or  
 CC metal, particularly for use as blood vessel or heart valve replacements,  
 CC wound or burn dressings, or stents. They can be used in cosmetic, elastic  
 CC or high-tensile strength materials, e.g. ropes or parachute cord.  
 CC Prostheses based on the MFU allow penetration of endothelial cells, so  
 CC become permanent, living, tissue replacements. The MFU polypeptides have  
 CC better biocompatibility than known elastin-based materials. They are well  
 CC defined, homogeneous material and are easier to manipulate and produce  
 CC than full-length elastins. They are non-thrombogenic and non-immunogenic.  
 CC Materials can be made from 2 or more different MFU polypeptides to allow  
 CC properties to be tailored for particular applications, e.g. combining the  
 CC high extensibility of elastin and the high tensile strength of spider  
 CC silk protein

XX SQ Sequence 730 AA;  
 Query Match 98.1%; Score 855.5; DB 2; Length 730;  
 Best Local Similarity 99.4%; Pred. No. 3.1e-56;  
 Matches 170; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 GVRRLSPRLREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGVG 60  
 Db 561 GVRRLSPRLREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGVG 620  
 QY 61 IPGGVVGAGPAAAAAKAAAKAAQFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPPAAAAK 120  
 Db 621 IPGGVVGAGPAAAAAKAAAKAAQFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPPAAAAK 680  
 QY 121 AAKYGAAGLGLGVGAGOFFLGGVAAPFGGLSPIFFGGACLGKACGRKK 171  
 Db 681 AAKYGAAGLGLGGA-QFPLGGVAAPFGGLSPIFFGGACLGKACGRKK 730

RESULT 13  
 AAY01311  
 ID AAY01311 standard; protein; 183 AA.  
 XX  
 AC AAY01311;  
 XX  
 DT 07-JUN-1999 (first entry)  
 DE Human tropoelastin derivative SHEL26-36 (excluding exon 26A product).  
 XX  
 KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9903886-A1.  
 XX  
 PD 28-JAN-1999.  
 XX  
 PF 17-JUL-1998; 98WO-AU000564.  
 XX  
 PR 18-JUL-1997; 97AU-00008117.  
 XX  
 PA (UNSY ) UNIV SYDNEY.  
 XX  
 PI Weiss AS;  
 XX  
 PS WPI; 1999-132162/11.  
 XX

XX New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.  
 XX  
 XX Claim 39; Page 11; 82pp; English.  
 XX  
 CC The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents a human  
 CC tropoelastin derivative SHEL26-36 excluding exon 26A product  
 XX  
 XX SQ Sequence 183 AA;  
 Query Match 83.1%; Score 725; DB 2; Length 183;  
 Best Local Similarity 97.3%; Pred. No. 5.4e-47;  
 Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 25 PSSPRVPGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVWAGPAAAAAKAAKAA 84  
 Db 37 PGFCAVPGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVWAGPAAAAAKAAKAA 96  
 QY 85 QFGLVGAAGLGLGVGGLGVGPGVGLGGLIPPPAAAAAKAAKYGAAGLGLGVGAGOFFLGGV 144  
 Db 97 QFGLVGAAGLGLGVGGLGVGPGVGLGGLIPPPAAAAAKAAKYGAAGLGLGVGAGOFFLGGV 156  
 QY 145 AARPGFGLSPIFFGGACLGKACGRKK 171  
 Db 157 AARPGFGLSPIFFGGACLGKACGRKK 183

RESULT 14  
 AAY69138  
 ID AAY69138 standard; protein; 183 AA.  
 XX  
 AC AAY69138;  
 XX  
 DT 30-MAY-2000 (first entry)  
 DE Amino acid sequence of a human tropoelastin derivative.  
 XX  
 KW Tropoelastin; derivative; proteolysis; protease; anti-wrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200004043-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 19-JUL-1999; 99WO-AU000580.  
 XX  
 PR 17-JUL-1998; 98AU-00004723.  
 XX  
 PA (UNSY ) UNIV SYDNEY.  
 XX  
 PI Weiss AS;  
 XX  
 DR WPI; 2000-182399/16.  
 XX  
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.  
 XX  
 PS Disclosure; Page 134-135; 136pp; English.  
 XX



The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility to proteolysis is used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives derived from protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

XX Sequence 183 AA;

Query Match 83.1%; Score 725; DB 3; Length 183;  
Best Local Similarity 97.3%; Pred. No. 5.4e-47;  
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSPRVPGALAAKAAKYGAAPVGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 84  
Db 37 PFGAVPGALAAKAAKYGAAPVGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 96

QY 85 QFGLVGAAGLGLGVGLGVPGVGGGLGIPPPAAAKAAKYGAAGLGVGLGGAGQPLGGV 144  
Db 97 QFGLVGAAGLGLGVGLGVPGVGGGLGIPPPAAAKAAKYGAAGLGVGLGGAGQPLGGV 156

QY 145 AARPGFGLSPIFFPGACLGKACGRKRK 171  
Db 157 AARPGFGLSPIFFPGACLGKACGRKRK 183

RESULT 15

AD40134  
ID AD40134 standard; protein; 692 AA.

AC ADE40134;

DT 29-JAN-2004 (first entry)

DE Human NOV16b protein - SEQ ID 40.

KW NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;  
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
KW tissue typing; human; NOV.

OS Homo sapiens.

XX WO2003064589-A2.

XX 07-AUG-2003.

XX 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

XX 03-AUG-2001; 2001US-0310291P.

XX 07-AUG-2001; 2001US-0310544P.

XX 08-AUG-2001; 2001US-0310951P.

XX 09-AUG-2001; 2001US-0311232P.

XX 13-AUG-2001; 2001US-0311979P.

XX 16-AUG-2001; 2001US-0312892P.

PR 17-AUG-2001; 2001US-0313201P.  
PR 17-AUG-2001; 2001US-0313415P.  
PR 20-AUG-2001; 2001US-0313643P.  
PR 20-AUG-2001; 2001US-0313702P.  
PR 21-AUG-2001; 2001US-0314031P.  
PR 23-AUG-2001; 2001US-0314466P.  
PR 28-AUG-2001; 2001US-0315403P.  
PR 29-AUG-2001; 2001US-0315853P.  
PR 17-SEP-2001; 2001US-0322716P.  
PR 21-SEP-2001; 2001US-0323994P.  
PR 14-DEC-2001; 2001US-0340233P.  
PR 05-FEB-2002; 2002US-0354591P.  
PR 19-MAR-2002; 2002US-0365478P.  
PR 19-APR-2002; 2002US-0373814P.  
PR 19-APR-2002; 2002US-0373825P.  
PR 19-APR-2002; 2002US-0373989P.  
PR 23-APR-2002; 2002US-0374632P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 01-AUG-2002; 2002US-00210172.

XX (CURA-) CURAGEN CORP.

PI Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK,

PI Shinkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;

PI Voss EZ, Boldog FL, Gorman L, Leite MM, Vernet CAM, Anderson DW;

PI Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;

PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DU;

PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;

PI Smithson G;

XX WPI: 2003-663472/62.

DR N-PSDB; ADE40133.

XX

PT New NOVX polypeptides and nucleic acids, useful for preventing or

PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,

PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX

PS Claim 1; SEQ ID NO 40; 560pp; English.

XX The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiasthmatic and gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.

XX Sequence 692 AA;

Query Match 83.1%; Score 725; DB 7; Length 692;

Best Local Similarity 97.3%; Pred. No. 1.9e-46;

Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSPRVPGALAAKAAKYGAAPVGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 84

Db 546 PFGAVPGALAAKAAKYGAAPVGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 605

QY 85 QFGLVGAAGLGLGVGLGVPGVGGGLGIPPPAAAKAAKYGAAGLGVGLGGAGQPLGGV 144

Db 606 QFGLVGAAGLGLGVGLGVPGVGGGLGIPPPAAAKAAKYGAAGLGVGLGGAGQPLGGV 665

QY 145 AARPGFGLSPIFFPGACLGKACGRKRK 171

Db 666 AARPGFGLSPIFFPGACLGKACGRKRK 692

Mon Nov 22 12:42:44 2004

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XX 30-MAY-2000 (first entry)
DT
XX Amino acid sequence of a human reduced tropoelastin derivative.
DE
XX
XX
XX Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease;
KW anti-wrinkle; hand lotion; bulking agent; chemotaxis; proliferation;
KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
KW metastasis; blood clotting.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO200004043-A1.
PN
XX
XX 27-JAN-2000.
PD
XX
XX 19-JUL-1999; 99WO-AU000580.
PF
XX
XX 17-JUL-1998; 98AU-00004723.
PR
XX
XX (UNSY ) UNIV SYDNEY.
PA
XX
XX Weiss AS;
PI
XX
XX WPI; 2000-182399/16.
DR
XX
XX N-PSDB; AAZ61144.
DR
XX
XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
PT cell growth.
PT
XX
XX Disclosure; Page 110-112; 136pp; English.
PS
XX
XX The present sequence represents a human reduced tropoelastin derivative,
CC designated SHEL-delta-26a. The sequence is produced by removing exon 26a
CC of SHEL (SHEL not defined). The protein is representative of tropoelastin
CC derivatives of the invention, in which a subsequence has been mutated so
CC that susceptibility to proteolysis is reduced or eliminated, or a
CC subsequence has been inserted so that susceptibility to proteolysis is
CC increased. The derivatives have with reduced susceptibility, and can be
CC used where the wild-type protein would be degraded too easily, e.g. in
CC contact with serum or wound exudate. The tropoelastin derivatives provide
CC competitive inhibition of protease activity. The tropoelastin
CC derivatives, and other polypeptides containing tropoelastin derivative-
CC derived protease-susceptibility sites, are useful in human or veterinary
CC medicine, cosmetics (e.g. anti-wrinkle or hand lotions), as bulking agents
CC and for inducing chemotaxis. They are also useful for proliferation or
CC growth inhibition, particularly of smooth muscle cells, epithelial or
CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
CC derivatives are competitive inhibitors of the protease, and are used for
CC protecting against lung damage caused by elastin, for inhibiting or
CC controlling localized growth of cancers or metastases, or to limit
CC protease activity that causes blood clotting
XX
XX Sequence 698 AA;
SQ
Query Match 83.1%; Score 725; DB 3; Length 698;
Best Local Similarity 97.3%; Pred. No. 1.9e-46;
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 25 PSSRPVPGALAAKAAKYGAAPVGLGGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 84
DB 552 PGFGAVPGALAAKAAKYGAAPVGLGGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 611
QY 85 QFGLVGAAGLGGVIGVPGVGLGGIIPAAAKAAKAAKYGAAGLGGVVGAGPPLGGV 144
DB 612 QFGLVGAAGLGGVIGVPGVGLGGIIPAAAKAAKAAKYGAAGLGGVVGAGPPLGGV 671
QY 145 AARPGFGLSPIFFGACGLGKACGRKK 171
DB 672 AARPGFGLSPIFFGACGLGKACGRKK 698
QY
DB
XX
XX AARPGFGLSPIFFGACGLGKACGRKK 171
DB 672 AARPGFGLSPIFFGACGLGKACGRKK 698
XX
XX AAY69069 standard; protein; 698 AA.
XX
XX AAY69069;
AC

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RESULT 18
AAO17360
ID AAO17360 standard; protein; 730 AA.
XX
AC AAO17360;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human elastin.
XX
KW Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
KW transmembrane receptor PTK7; collagen type XVIII alpha 1;
KW platelet derived growth factor receptor alpha; laminin M chain;
KW subtilisin like protein PACE4; nidogen.
XX
OS Homo sapiens.
XX
PN EF1191107-A2.
XX
PD 27-MAR-2002.
XX
PF 21-AUG-2001; 2001EP-00250300.
XX
PR 25-SEP-2000; 2000DE-01048633.
XX
PA (SCHD ) SCHERING AG.
XX
PI Hess-Stumpp H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;
PI Regidor P, Scotti S;
XX
WPI; 2002-317413/36.
XX
PT In vitro diagnosis and monitoring of endometriosis, comprises detecting
PT reduced expression of specific gene products, e.g. from the fibronectin
PT gene.
XX
PS Claim 1; Page 15-16; 2lpp; German.
XX
CC The present invention relates to a method for the in vitro diagnosis of
CC endometriosis by determining the amount of gene product from at least one
CC specific gene in a patient sample and comparing this with the amount of
CC gene product in a control sample. A reduced level is indicative of
CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
CC transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet
CC derived growth factor receptor alpha, laminin M chain, subtilisin like
CC protein PACE4 or nidogen. The method is useful for initial diagnosis of
CC endometriosis, and also for monitoring progress and treatment of the
CC disease. The present sequence is human elastin
XX
SQ Sequence 730 AA;

Query Match      83.1%; Score 725; DB 5; Length 730;
Best Local Similarity 97.3%; Pred. No. 2e-46;
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSRVPGALAAAKAAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAAAATAAKAA 84
DB 584 PGFGAVPGALAAAKAAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAAAATAAKAA 643
QY 85 QFGLVGAAGLGGVIGPGVVGGLGIPPAATAAKAAYGAAAGLGGVVGAGPPLGGV 144
DB 644 QFGLVGAAGLGGVIGPGVVGGLGIPPAATAAKAAYGAAAGLGGVVGAGPPLGGV 703
QY 145 AARPGFGLSPFPFGACLGKACGRKRK 171
DB 704 AARPGFGLSPFPFGACLGKACGRKRK 730

RESULT 20
AAO1304
ID AAY01304 standard; protein; 147 AA.
XX
AC AAY01304;

```

RESULT 19  
 ADQ19747  
 ID ADQ19747 standard; protein; 730 AA.  
 XX  
 AC ADQ19747;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.  
 XX  
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004048938-A2.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 26-NOV-2003; 2003WO-US038193.  
 XX  
 PR 26-NOV-2002; 2002US-0429739P.  
 XX  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Aziz N, Ginsburg WM, Zlotnik A;  
 XX  
 WPI; 2004-441208/41.  
 XX  
 PT Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 XX  
 PS Example 2; SEQ ID NO 2566; 210pp; English.  
 XX  
 CC The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytostatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 CC acid sequences may be useful in diagnostic and screening applications.  
 CC The current sequence is that of a human soft tissue sarcoma-upregulated  
 CC protein of the invention. The current sequence is not shown within the  
 CC specification per se but was submitted in CD format by the inventor.  
 XX  
 SQ Sequence 730 AA;

Query Match 83.1%; Score 725; DB 8; Length 730;  
 Best Local Similarity 97.3%; Pred. No. 2e-46;  
 Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSRVPGALAAAKAAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAAAATAAKAA 84  
 DB 584 PGFGAVPGALAAAKAAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAAAATAAKAA 643  
 QY 85 QFGLVGAAGLGGVIGPGVVGGLGIPPAATAAKAAYGAAAGLGGVVGAGPPLGGV 144  
 DB 644 QFGLVGAAGLGGVIGPGVVGGLGIPPAATAAKAAYGAAAGLGGVVGAGPPLGGV 703  
 QY 145 AARPGFGLSPFPFGACLGKACGRKRK 171  
 DB 704 AARPGFGLSPFPFGACLGKACGRKRK 730

RESULT 20  
 AAY01304  
 ID AAY01304 standard; protein; 147 AA.  
 XX  
 AC AAY01304;

XX  
DT 07-JUN-1999 (first entry)  
XX DE Human tropoelastin derivative SHELGamma.  
XX OS Homo sapiens.  
XX PN EP1347046-A1.  
KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
XX OS Homo sapiens.  
OS Synthetic.  
XX WO9903886-A1.  
PN 28-JAN-1999.  
PD XX  
PF 17-JUL-1998; 98WO-AU000564.  
PP XX  
PR 18-JUL-1997; 97AU-00008117.  
PX (UNSY) UNIV SYDNEY.  
PY PA  
PZ Weiss AS;  
PI PI  
PT PT  
DR WPI; 1999-132162/11.  
DR N-PSDB; AAX27706.  
XX New derivatives of human tropoelastin - with elastin-like or  
XX macromolecular binding properties, useful e.g. as surgical implants.  
XX Claim 19; Fig 7; 82pp; English.  
XX The invention relates to a derivative or variant of human tropoelastin  
CC (hTE) having elasin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives  
CC or hybrid proteins containing the derivatives are useful in medical,  
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26A, from hTE. The present sequence represents a human  
CC tropoelastin derivative SHELGamma excluding the product encoded by exon  
CC 26A  
XX SQ Sequence 147 AA;  
Query Match 82.9%; Score 723; DB 2; Length 147;  
Best Local Similarity 100.0%; Pred. No. 6.2e-47; Indels 0; Gaps 0;  
Matches 142; Conservative 0; Mismatches 0;  
QY 30 VPGALAAAKAYCAAVPGVGLGGLGAGVGIPGGVVGAGPAAAAAKAAKAAQFGILV 89  
Db 6 VPGLAAAKAAKYGAAPGVGLGGLGAGVGIPGGVVGAGPAAAAAKAAKAAQFGILV 65  
QY 90 GAAGLGLGVGVLGPVPGVGLGIGIPPAKAAKAYGAAGLVGAGGFPLGGVAARPG 149  
Db 66 GAAGLGLGVGVLGPVPGVGLGIGIPPAKAAKAYGAAGLVGAGGFPLGGVAARPG 125  
QY 150 FGLSPFPGACLCGCKGRKK 171  
Db 126 FGLSPFPGACLCGCKGRKK 147  
RESULT 21  
ADM03792 ID ADM03792 standard; protein; 663 AA.  
XX AC ADM03792;  
XX DT 20-MAY-2004 (first entry)

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OS Homo sapiens.
OS Synthetic.
PN WO9903886-A1.
XX
PD 28-JAN-1999.
XX
XX 17-JUL-1998; 98WO-AU000564.
PF
PR 18-JUL-1997; 97AU-00008117.
XX
XX (UNSY ) UNIV SYDNEY.
PA
XX Weiss AS;
PI
DR WPI; 1999-132162/11.
DR N-PSDB; AAX27705.
XX
XX New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
PT
XX Claim 7; Fig 3; 82pp; English.
XX
XX The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents a human
CC tropoelastin derivative SHEDdelta modified
XX
SQ Sequence 660 AA;

Query Match
Best Local Similarity 81.5%; Score 710.5; DB 2; Length 660;
Matches 142; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 25 PSSRPVPGALAAAKAAYGAAPVGLGGLGAGVIGPGVVGAGPAAAKAAKAAKAA 84
Db 515 PFGGAVPGALAAAKAAYG-AVPGVGLGGLGAGVIGPGVVGAGPAAAKAAKAAKAA 573
QY 85 QFGLVGAAGLGLGVLGVLGPGVGLGGLGTPPAAAKAAYGAAGLGGVGLGGAGQFPLGGV 144
Db 574 QFGLVGAAGLGLGVLGVLGPGVGLGGLGTPPAAAKAAYGAAGLGGVGLGGAGQFPLGGV 633
QY 145 AARPGFGLSPIPPGACILGKACGRKRK 171
Db 634 AARPGFGLSPIPPGACILGKACGRKRK 660

RESULT 23
ADB64761
ID ADB64761 standard; protein; 617 AA.
XX
AC ADB64761;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human protein encoded by clone NT2RP70003110.
DE
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
OS Homo sapiens.
XX
PN EP1308459-A2.

```

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XX
PD 07-MAY-2003.
XX
XX 28-MAR-2002; 2002EP-00007401.
PF
XX 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR N-PSDB; ADB62791.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
PT
XX Claim 1; Page; 222pp; English.
XX
XX The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 617 AA;

Query Match
Best Local Similarity 70.2%; Score 612; DB 7; Length 617;
Matches 125; Conservative 0; Mismatches 4; Indels 18; Gaps 1;

QY 25 PSSRPVPGALAAAKAAYGAAPVGLGGLGAGVIGPGVVGAGPAAAKAAKAAKAA 84
Db 489 PFGGAVPGALAAAKAAYGAAPVGLGGLGAGVIGPGVVGAGPAAAKAAKAAKAA 548
QY 85 QFGLVGAAGLGLGVLGVLGPGVGLGGLGTPPAAAKAAYGAAGLGGVGLGGAGQFPLGGV 144
Db 549 QFGLVGAAGLGLGVLGVLGPGVGLGGLGTPPAAAKAAYGAAGLGGVGLGGAGQFPLGGV 590
QY 145 AARPGFGLSPIPPGACILGKACGRKRK 171
Db 591 AARPGFGLSPIPPGACILGKACGRKRK 617

RESULT 24
AAB08630
ID AAB08630 standard; peptide; 712 AA.
XX
XX AAB08630;
AC

```

DT 20-DEC-2000 (first entry)  
XX Fusion protein comprising human elastin and c-myc.  
DE  
XX  
XX Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;  
KW smooth muscle cell differentiation; smooth muscle cell migration;  
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;  
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;  
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;  
KW SVAS; hypertension; transplant arteriopathy.  
XX  
XX Synthetic.  
OS Homo sapiens.  
OS Unidentified.  
XX  
XX WO200050068-A2.  
XX  
XX 31-AUG-2000.  
XX  
XX 28-FEB-2000; 2000WO-US002526.  
XX  
XX 26-FEB-1999; 99US-00258217.  
XX  
XX (UTAH ) UNIV UTAH RES FOUND.  
XX  
XX Keating MT, Li DY;  
XX  
XX WPI; 2000-533134/48.  
XX  
XX Elastin based compositions useful for treating atherosclerosis,  
PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,  
PT aneurysm, dissection SVAS and/or hypertension.  
XX  
XX Example 3; Page 48; 79pp; English.  
XX  
XX The present sequence represents a fusion protein, comprising human  
CC elastin and c-myc, preceded by a His tag. The protein is used in  
CC compositions of the invention. The specification describes elastin based  
CC compositions that are potent regulators of smooth muscle cell  
CC proliferation, differentiation and migration in vivo. The elastin-based  
CC tropoelastins (or fragments of them) which have biological activities  
CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;  
CC stimulating the differentiation of smooth muscle cells in vivo; and  
CC regulating the migration of smooth muscle cells in vivo. The compositions  
CC may be used for the prophylaxis or treatment of a disorder characterized  
CC by diminished capacity to regulate smooth muscle cell function such as  
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant  
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated  
CC also include SVAS (undefined), hypertension, and transplant arteriopathy  
XX  
XX Sequence 730 AA;  
Query Match 70.2%; Score 612; DB 3; Length 730;  
Best Local Similarity 85.0%; Pred. No. 6.2e-38;  
Matches 125; Conservative 0; Mismatches 4; Indels 18; Gaps 1;  
QY 25 PSSPRVPCALAAAKAAYGAAPVGLGGLGALGVGIPGVGAGPAAAAAAXAA 84  
DB 593 PFGAVPGALAAAKAAYGAAPVGLGGLGALGVGIPGVGAGPAAAAAAXAA 652  
QY 85 QFGLVGAAGLGLGVGGLGVGVPVGLGIPPAATAAKAAYGAAGLGVGAGPPLGGV 144  
DB 653 QFGLVGAAGLGLGVGGLGVGVPVGLGIPPAATAAKAAYGAAGLGVGAGPPLGGV 694  
QY 145 AARPGFGLSPIPPGACLGKACGRKRK 171  
DB 695 AARPGFGLSPIPPGACLGKACGRKRK 721  
RESULT 26  
ADE40132  
ID ADE40132 standard; protein; 711 AA.  
XX

XX  
DT 20-DEC-2000 (first entry)  
XX Amino acid sequence of a human elastin polypeptide.  
DE  
XX  
XX Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;  
KW smooth muscle cell differentiation; smooth muscle cell migration;  
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;  
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;  
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;  
KW SVAS; hypertension; transplant arteriopathy.  
XX  
XX Homo sapiens.  
XX  
XX WO200050068-A2.  
XX  
XX 31-AUG-2000.  
XX  
XX 28-FEB-2000; 2000WO-US002526.  
XX  
XX 26-FEB-1999; 99US-00258217.  
XX  
XX (UTAH ) UNIV UTAH RES FOUND.  
XX  
XX Keating MT, Li DY;  
XX  
XX WPI; 2000-533134/48.  
XX  
XX Elastin based compositions useful for treating atherosclerosis,  
PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,  
PT aneurysm, dissection SVAS and/or hypertension.  
XX  
XX Example 3; Page 46; 79pp; English.  
XX  
XX The present sequence represents a human elastin. Peptides derived from  
CC elastin are used in compositions of the invention. The specification  
CC describes elastin based compositions that are potent regulators of smooth  
CC muscle cell proliferation, differentiation and migration in vivo. The  
CC elastin-based compositions comprise at least one elastic fibre, elastins,  
CC tropoelastins (or fragments of them) which have biological activities  
CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;  
CC stimulating the differentiation of smooth muscle cells in vivo; and  
CC regulating the migration of smooth muscle cells in vivo. The compositions  
CC may be used for the prophylaxis or treatment of a disorder characterized  
CC by diminished capacity to regulate smooth muscle cell function such as  
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant  
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated  
CC also include SVAS (undefined), hypertension, and transplant arteriopathy  
XX  
XX Sequence 712 AA;  
Query Match 70.2%; Score 612; DB 3; Length 712;  
Best Local Similarity 85.0%; Pred. No. 6.1e-38;  
Matches 125; Conservative 0; Mismatches 4; Indels 18; Gaps 1;  
QY 25 PSSPRVPCALAAAKAAYGAAPVGLGGLGALGVGIPGVGAGPAAAAAAXAA 84  
DB 584 PFGAVPGALAAAKAAYGAAPVGLGGLGALGVGIPGVGAGPAAAAAAXAA 643  
QY 85 QFGLVGAAGLGLGVGGLGVGVPVGLGIPPAATAAKAAYGAAGLGVGAGPPLGGV 144  
DB 644 QFGLVGAAGLGLGVGGLGVGVPVGLGIPPAATAAKAAYGAAGLGVGAGPPLGGV 685  
QY 145 AARPGFGLSPIPPGACLGKACGRKRK 171  
DB 686 AARPGFGLSPIPPGACLGKACGRKRK 712  
RESULT 25  
AAB08631  
ID AAB08631 standard; peptide; 730 AA.  
XX  
XX AAB08631;  
AC  
XX







```

XX PA (UNSY ) UNIV SYDNEY.
XX PI Weiss AS;
XX XX WPI; 1999-132162/11.
XX XX
XX PT New derivatives of human tropoelastin - with elastin-like or
XX PT macromolecular binding properties, useful e.g. as surgical implants.
XX XX
XX PS Claim 23; Page 10; 82pp; English.
XX XX
XX CC The invention relates to a derivative or variant of human tropoelastin
XX CC (hTE) having elastin-like and/or macromolecule (specifically
XX CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX CC comprising the nucleic acids encoding the variants or derivatives are
XX CC used to produce the proteins recombinantly. The tropoelastin derivatives
XX CC or hybrid proteins containing the derivatives are useful in medical,
XX CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX CC wrinkle or hand lotions, also as surgical implants, foods and industrial
XX CC products. The hybrid protein have controllable GAG-binding properties,
XX CC depending on presence or absence of a specific fragment, designated
XX CC peptide 26A, from hTE. The present sequence represents a human
XX CC tropoelastin derivative SHEL31-36
XX XX
XX SQ Sequence 60 AA;
XX
Query Match 36.5%; Score 318; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 7.4e-17;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 112 GTPPAAAAAAYGAAGLVGGAGQFFPLGGVAARPFGFLSPIPPGGACLGKACGRKK 171
DB 1 GTPPAAAAAAYGAAGLVGGAGQFFPLGGVAARPFGFLSPIPPGGACLGKACGRKK 60
XX
RESULT 30
ID AAB88422
XX
AC AAB88422;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSEC0191.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
XX KW rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
FN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
FR 08-JUL-1999; 99JP-00194179.
XX
PR 11-JAN-2000; 2000JP-00118775.
XX
PR 02-MAY-2000; 2000JP-00183766.
XX
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR WPI; 2001-093989/11.
XX
DR N-FSDB; AAF93849.
XX
XX
XX PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX PT gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
XX

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CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbant assay (ELISA)). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX
XX SQ Sequence 472 AA;
XX
Query Match 32.1%; Score 280; DB 4; Length 472;
Best Local Similarity 34.7%; Pred. No. 3.7e-13;
Matches 90; Conservative 13; Mismatches 28; Indels 128; Gaps 12;
XX
QY 25 PSSRPVPGALAAKAAKYGAAPVGVGLGALGGVIGPGVVGAGPAAAA----- 74
DB 62 PLKP-VPGGLAGA-----GLGAGLGLGGVIGPGVVGAGPAAAAAAKAAKYG 110
QY 75 -----AAAKAA 80
DB 111 AAAGLVPGGPGFGVGVPGAGVPGVPGAGIPVPGAGIPGAAPGVGVSPEAAAKAA 170
QY 81 AKAAQFGLVGAAGLGL-----GVGGL-----GVPGVG-----GLGGIP----- 114
DB 171 AKAAKYGARPGVGVGGIPTYGVGAGGFGFGVGVGGIPGVAGVPGVGVGGVPGVGI 230
QY 115 -----PAAAAKAAKYG-----AAGLG-----GVLGGAGQFPLGGVAARPFGFLSP----- 154
DB 231 SPEAQAATAAAKAAKYGLVPGVGVAPFGVGVAPGVGVLAP--GVGVAPGVGVAPGVG 288
QY 155 -----IFPGG-ACLGKACGR 168
DB 289 VAPGIGPGVAAAKSAK 307
XX
Search completed: November 19, 2004, 16:28:45
Job time : 37.9467 secs

```



Result No.	Score	Query		DB	ID	Description
		Match	%			
1	872	100.0	731	10	US-09-964-662-1	Sequence 1, Appli
2	725	83.1	692	15	US-10-210-172-40	Sequence 40, Appl
3	725	83.1	730	10	US-09-961-403-8	Sequence 8, Appli
4	717	82.2	663	15	US-10-108-260A-2477	Sequence 2477, Ap
5	612	70.2	617	14	US-10-104-047-2915	Sequence 2915, Ap
6	609	69.8	711	15	US-10-210-172-38	Sequence 38, Appl
7	216.5	24.8	144	15	US-10-424-599-269890	Sequence 269890,
8	212.5	24.4	199	10	US-09-964-662-11	Sequence 11, Appl
9	212.5	24.4	200	10	US-09-964-662-2	Sequence 2, Appli
10	195.5	22.4	641	14	US-10-138-098-52	Sequence 52, Appl
11	195.5	22.4	641	14	US-10-294-804-4	Sequence 4, Appli
12	195.5	22.4	641	14	US-10-225-838B-22	Sequence 22, Appl
13	195.5	22.4	641	16	US-10-732-694-11	Sequence 11, Appl

```
87      167      19.2      2368      14      US-10-141-756-423      Sequence 423, App
88      167      19.2      2368      14      US-10-141-753-423      Sequence 423, App
89      167      19.2      2368      14      US-10-140-805-423      Sequence 423, App
90      167      19.2      2368      14      US-10-140-864-423      Sequence 423, App
91      167      19.2      2368      15      US-10-142-426-423      Sequence 423, App
92      165.5      19.0      525      15      US-10-282-122A-64763      Sequence 64763, A
93      165.5      19.0      1670      14      US-10-123-155-325      Sequence 325, App
94      165.5      19.0      1670      14      US-10-146-731-325      Sequence 325, App
95      165.5      19.0      1670      14      US-10-140-472-325      Sequence 325, App
96      165.5      19.0      1670      14      US-10-141-761-325      Sequence 325, App
97      165.5      19.0      1670      14      US-10-142-885-325      Sequence 325, App
98      165.5      19.0      1670      14      US-10-158-790-325      Sequence 325, App
99      165.5      19.0      1670      14      US-10-137-871-325      Sequence 325, App
100     165.5      19.0      1670      14      US-10-140-923-325      Sequence 325, App
```

ALIGNMENTS

```
RESULT 1
US-09-964-662-1
; Sequence 1, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD
; TITLE OF INVENTION: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-662-1
```

```
Query Match      100.0%; Score 872; DB 10; Length 731;
Best Local Similarity 100.0%; Pred. No. 3e-55;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      GVRRLSPRLREGDPSSQHLPTSPSSRPVPGALAAKAAKYGAAPVGLGGLGALGVG 60
Db      561     GVRRLSPRLREGDPSSQHLPTSPSSRPVPGALAAKAAKYGAAPVGLGGLGALGVG 620

Qy      61      IPGVGVGAPAAAATAKAAKAAQFGLVGAAGLGLGVGPGVGLGIPPAATAK 120
Db      621     IPGVGVGAPAAAATAKAAKAAQFGLVGAAGLGLGVGPGVGLGIPPAATAK 680

Qy      121     AAKYGAAGLGLGVGAGOFFLGGVAARPFGLSPIFFPGACILGKACGRKK 171
Db      681     AAKYGAAGLGLGVGAGOFFLGGVAARPFGLSPIFFPGACILGKACGRKK 731
```

```
RESULT 2
US-10-210-172-40
; Sequence 40, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerrhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigar, Muralidhara
```

```
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Marlo
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalte, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 40
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-40

Query Match      83.1%; Score 725; DB 15; Length 692;
Best Local Similarity 97.3%; Pred. No. 1.3e-44;
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      25      PSSRPVPCALAAKAAKYGAAPVGLGGLGALGVGIPGVVGVGAPAAAATAKAAKAA 84
Db      546     PGFAGVPGALAAKAAKYGAAPVGLGGLGALGVGIPGVVGVGAPAAAATAKAAKAA 605

Qy      85      QFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPAATAKAAKYGAAGLGGVGLGAGOFFLGGV 144
Db      606     QFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPAATAKAAKYGAAGLGGVGLGAGOFFLGGV 665

Qy      145     AARPFGLSPIFFPGACILGKACGRKK 171
Db      666     AARPFGLSPIFFPGACILGKACGRKK 692

RESULT 3
US-09-961-403-8
; Sequence 8, Application US/09961403
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 7.69127 Seconds  
(without alignments)  
2139.198 Million cell updates/sec

Title: US-09-743-818A-73

Perfect score: 872

Sequence: 1 GVRSLSPDLREGDPSSSQH.....LSPIFFGGACLGKACGRKK 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	872	100.0	792	1 EAHU	elastin precursor,
2	509	58.4	770	2 S59623	tropoelastin - she
3	483.5	56.1	860	1 EAMS	elastin precursor
4	486	55.7	747	1 EABO	elastin precursor
5	482	55.3	864	1 EART	elastin precursor
6	290.5	33.3	784	2 A26601	elastin precursor
7	195.5	22.4	641	1 QQBE31	nuclear antigen EB
8	194.5	22.3	718	2 A36068	major amputate fi
9	191	21.9	268	2 B61615	fibroin heavy chai
10	190	21.8	767	2 E70895	hypothetical glyci
11	184	21.1	783	2 T35389	probable serine-th
12	181	20.8	162	2 S56703	glycine-rich cell
13	178.5	20.5	741	2 G70917	hypothetical glyci
14	178.5	20.5	1329	2 E70917	hypothetical glyci
15	175.5	20.1	1901	2 F70806	hypothetical glyci
16	173.5	19.9	158	2 T08957	glycine-rich prote
17	172.5	19.8	1489	2 D70807	hypothetical glyci
18	172	19.7	749	2 A70812	hypothetical glyci
19	171.5	19.7	618	2 A70989	hypothetical glyci
20	171	19.6	667	2 A70893	hypothetical glyci
21	170.5	19.6	603	2 A70770	hypothetical glyci
22	170.5	19.6	615	2 A70589	hypothetical glyci
23	170	19.5	212	2 E86179	hypothetical glyci
24	170	19.5	882	2 B70812	hypothetical prote
25	169.5	19.4	2639	2 T31328	hypothetical glyci
26	168	19.3	907	2 A45560	fibroin - Chinese
27	167	19.2	256	2 A70514	sporozoite surface
28	167	19.2	627	2 A44112	hypothetical glyci
29	167	19.2	837	2 E70835	spidroin 2, dragli
30	167	19.2	142	1 JBAA041	hypothetical glyci
31	165.5	19.0	525	2 E70806	hypothetical glyci
32	165	18.9	778	2 F70878	hypothetical glyci
33	163.5	18.8	801	2 F70824	hypothetical glyci
34	163.5	18.8	957	2 D70835	hypothetical glyci
35	163.5	18.8	1660	2 A70869	hypothetical glyci
36	162.5	18.6	515	2 H70663	hypothetical glyci
37	161.5	18.5	384	1 A26099	glycine-rich cell
38	161.5	18.5	491	2 D70916	hypothetical glyci
39	161	18.5	498	2 C70720	hypothetical glyci
40	161	18.5	914	2 H70987	hypothetical glyci
41	160	18.3	783	2 E70824	hypothetical glyci
42	159.5	18.3	1538	2 H70846	hypothetical glyci
43	159	18.2	606	2 H70816	hypothetical glyci
44	159	18.2	1306	2 A70934	hypothetical glyci
45	157.5	18.1	419	2 G70602	hypothetical glyci
46	157	18.0	584	2 F70804	hypothetical prote
47	157	18.0	694	2 F70868	hypothetical glyci
48	156.5	17.9	439	2 D70954	hypothetical glyci
49	156	17.9	496	2 H70839	hypothetical glyci
50	155.5	17.8	245	2 F70787	hypothetical glyci
51	154	17.7	812	2 S31521	hypothetical glyci
52	154	17.7	1669	1 CGMS4B	collagen COLF1 - f
53	153.5	17.6	479	2 F70573	hypothetical glyci
54	153.5	17.6	591	2 B70523	hypothetical glyci
55	153	17.5	562	2 B70953	hypothetical glyci
56	152	17.4	576	2 A70900	hypothetical glyci
57	152	17.4	743	1 S23779	hypothetical glyci
58	152	17.4	964	1 CGCH2S	collagen alpha 1V
59	152	17.4	1079	2 B70807	collagen alpha 2(I
60	151	17.3	1669	1 CGHU4B	collagen alpha 1(I
61	151	17.3	1763	2 S16366	collagen alpha 2(I
62	150.5	17.3	1414	1 S23809	collagen alpha 1(I
63	149.5	17.1	673	1 CGB06C	collagen alpha 1(I
64	149.5	17.1	681	2 AB2155	hypothetical prote
65	149.5	17.1	730	2 A36226	collagen alpha 1 c
66	149.5	17.1	744	2 S15435	collagen alpha 1V
67	149.5	17.1	923	2 E70820	hypothetical glyci
68	149	17.1	754	2 A5267	collagen alpha 5(I
69	149	17.1	1466	1 CGHU7L	collagen alpha 1(I
70	148.5	17.0	1418	2 T45467	collagen alpha 1(I
71	148	17.0	487	2 E70983	hypothetical glyci
72	148	17.0	931	2 S13580	collagen alpha 1(I
73	147	16.9	201	2 T00799	hypothetical prote
74	147	16.9	463	2 B70893	hypothetical glyci
75	147	16.9	731	2 C70974	hypothetical glyci
76	147	16.9	1373	1 A43291	collagen alpha 2(I
77	146.5	16.8	112	2 JQ1063	glycine-rich prote
78	146.5	16.8	301	2 B31219	collagen 2 - Caeno
79	146.5	16.8	532	2 F70580	hypothetical glyci
80	146.5	16.8	1487	1 CGHU6C	collagen alpha 1(I
81	146	16.7	87	2 T14302	glycine-rich cell
82	146	16.7	402	1 CGB02S	collagen alpha 2(I
83	145.5	16.7	356	2 S16907	collagen alpha 1(I
84	145.5	16.7	447	2 G84687	probable disease x
85	145.5	16.7	853	2 A70896	hypothetical glyci
86	145.5	16.7	1366	1 CGHU2S	collagen alpha 2(I
87	145.5	16.7	1419	2 A41182	collagen alpha 1(I
88	145.5	16.7	1487	2 B41182	collagen alpha 1(I
89	145	16.6	1758	2 T29350	hypothetical prote
90	145	16.6	1759	2 T29351	collagen alpha 2(I
91	144.5	16.6	457	2 H70820	hypothetical glyci
92	144.5	16.6	588	2 F70971	hypothetical glyci
93	144.5	16.6	635	2 A57131	collagen alpha 2(V
94	144.5	16.6	839	2 F75518	hypothetical prote
95	144	16.5	461	2 F70571	hypothetical glyci
96	143.5	16.5	361	2 G70682	hypothetical glyci
97	143.5	16.5	401	1 QZQAC	circumsporozoite p
98	142.5	16.3	744	1 A34246	collagen alpha 1(V
99	142.5	16.3	744	1 S23298	collagen alpha 1(V
100	142	16.3	171	1 JBAA041	chorion class B pr

## RESULT 2

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 34.5734 Seconds  
(without alignments)  
2845.805 Million cell updates/sec

Title: US-09-743-818A-73

Perfect score: 872

Sequence: 1 GVRSLSPRLREGDPSSSH.....LSPIPPGGACLGKACGRKRK 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	872	100.0	757	2	Q14234	Q14234 homo sapien
2	872	100.0	757	2	Q75MU5	Q75mu5 homo sapien
3	872	100.0	757	2	AAS07435	AAS07435 homo sapi
4	725	83.1	258	2	Q9UMF5	Q9umf5 homo sapien
5	725	83.1	730	1	ELIS_HUMAN	ELIS_HUMAN
6	720	82.6	643	2	Q8NB14	Q8nb14 homo sapien
7	612	70.2	570	2	Q6ZMJ6	Q6zwm6 homo sapien
8	612	70.2	570	2	BAC85506	BAC85506 homo sapi
9	612	70.2	658	2	Q6POL4	Q6p0l4 homo sapien
10	612	70.2	658	2	AAH65566	AAH65566
11	612	70.2	687	2	Q14235	Q14235 homo sapien
12	608	69.7	687	2	Q7Z316	Q7z316 homo sapien
13	605	69.4	711	2	Q7Z3F5	Q7z3f5 homo sapien
14	531.5	61.0	707	2	Q28098	Q28098 bos taurus
15	489.5	56.1	810	2	Q28098	Q28098 bos taurus
16	489.5	56.1	860	1	ELIS_MOUSE	ELIS_MOUSE
17	489.5	56.1	860	2	Q8C9L8	Q8c9l8 mus musculu
18	485	55.6	666	2	Q28096	Q28096 mus musculu
19	482	55.3	864	1	ELIS_RAT	ELIS_RAT
20	477	54.7	747	1	ELIS_BOVIN	ELIS_BOVIN
21	442	50.7	679	2	Q28097	Q28097 bos taurus
22	436	50.0	650	2	Q28099	Q28099 bos taurus
23	295.5	33.9	750	1	ELIS_CHICK	ELIS_CHICK
24	295	33.8	100	1	ELIS_SHEEP	ELIS_SHEEP
25	280	32.1	472	2	Q8N2G0	Q8n2g0 homo sapien
26	273.5	31.4	602	2	O15337	O15337 homo sapien
27	273.5	31.4	635	2	O15336	O15336 homo sapien
28	269	30.8	559	2	Q6ZUN2	Q6zun2 homo sapien
29	269	30.8	559	2	BAC86188	BAC86188 homo sapi
30	213.5	24.5	1468	2	Q9GUB5	Q9gub5 gallieria me
31	204	23.4	738	2	O02402	O02402 pinctada fu

32	201	23.1	644	2	Q8WSW4	Q8wsW4 nephila cla
33	199	22.8	544	2	O46171	O46171 nephila cla
34	195.5	22.4	641	1	EBN1_EBV	R03211 epstein-bar
35	195.5	22.4	641	2	Q777E1	Q777e1 human herpe
36	195.5	22.4	641	2	CAD53427	Cad53427 human her
37	195	22.4	443	2	Q9GUB4	Q9gub4 gallieria me
38	195	22.4	1002	2	Q9BIU8	Q9biu8 argiope tri
39	194.5	22.3	747	1	SPD1_NBPCL	P19837 nephila cla
40	194	22.2	617	2	O46172	O46172 nephila cla
41	194	22.2	651	2	Q9BIU9	Q9biu9 argiope tri
42	193.5	22.2	294	2	Q16986	Q16986 araneus dia
43	193	22.1	691	2	Q9BIU3	Q9biu3 dolomedes t
44	191	21.9	268	2	O7M468	O7m468 gallieria me
45	191	21.9	648	2	Q9BIU7	Q9biu7 argiope tri
46	190	21.8	767	2	Q79FT0	Q79ft0 mycobacteri
47	190	21.8	767	2	CAE55354	CAE55354 mycobacte
48	190	21.8	774	2	Q7U0P7	Q7u0p7 mycobacteri
49	189.5	21.7	172	2	Q9BDZ0	Q9bdz0 macaca mula
50	189	21.7	447	2	Q9BIU1	Q9biu1 argiope aur
51	187.5	21.5	69	2	Q28101	Q28101 bos taurus
52	187.5	21.5	1460	2	Q7TWC3	Q7twc3 mycobacteri
53	185	21.2	524	2	Q817U1	Q817u1 araneus ven
54	184	21.1	783	2	Q9XAI1	Q9xai1 streptomyce
55	183.5	21.0	988	2	O17434	O17434 nephila cla
56	182	20.9	563	2	Q6J6N0	Q6j6n0 araneus ven
57	182	20.9	563	2	AAT36347	Aat36347 araneus v
58	182	20.9	904	2	Q76271	Q76271 mytilus edu
59	181	20.8	162	2	Q39691	Q39691 daucus caro
60	180.5	20.7	349	2	Q9BIU0	Q9biu0 argiope aur
61	178.5	20.5	738	2	O8VK15	O8vk15 mycobacteri
62	178.5	20.5	741	2	Q79FPI	Q79fpl mycobacteri
63	178.5	20.5	741	2	CAE55391	CAE55391 mycobacte
64	178.5	20.5	795	2	Q7U020	Q7u020 mycobacteri
65	178.5	20.5	1329	2	Q79FP2	Q79fp2 mycobacteri
66	178.5	20.5	1329	2	CAE55390	CAE55390 mycobacte
67	177.5	20.4	2655	2	Q964F4	Q964f4 antheraea y
68	177	20.3	905	2	Q8MW55	Q8mw55 mytilus gal
69	176.5	20.2	233	2	Q9BIT6	Q9bit6 nephila ina
70	176.5	20.2	253	2	Q9BIT4	Q9bit4 nephila sen
71	176.5	20.2	922	2	Q8MW53	Q8mw53 mytilus gal
72	175.5	20.1	1715	2	Q8VI20	Q8vizo mycobacteri
73	175.5	20.1	1901	1	PG54_MYCTU	O53553 mycobacteri
74	174.5	20.0	342	2	Q9BIU1	Q9biu1 gasteracant
75	174.5	20.0	922	2	O44367	O44367 mytilus edu
76	174	20.0	373	2	Q9BIT9	Q9bit9 latrodectus
77	174	20.0	603	2	Q7U079	Q7u079 mycobacteri
78	174	20.0	1360	2	Q7TWC4	Q7twc4 mycobacteri
79	174	20.0	1408	2	Q7U022	Q7u022 mycobacteri
80	173.5	19.9	158	2	Q9SZD2	Q9szd2 arabidopsis
81	173	19.8	486	2	Q9AR23	Q9ar23 oryza sativ
82	172.5	19.8	360	2	Q9BIU0	Q9biu0 latrodectus
83	172.5	19.8	1489	2	Q6MMW6	Q6mmw6 mycobacteri
84	172.5	19.8	1489	2	CAE55607	CAE55607 mycobacte
85	172	19.7	749	2	Q7D974	Q7d974 mycobacteri
86	172	19.7	749	2	Q79FV7	Q79fv7 mycobacteri
87	172	19.7	749	2	CAE55328	CAE55328 mycobacte
88	172	19.7	773	2	Q7U160	Q7u160 mycobacteri
89	171.5	19.7	618	2	Q79FK9	Q79fk9 mycobacteri
90	171.5	19.7	618	2	CAE55419	CAE55419 mycobacte
91	171	19.6	399	2	Q9BIT8	Q9bit8 latrodectus
92	171	19.6	667	2	Q7D8W7	Q7d8w7 mycobacteri
93	171	19.6	667	2	Q79FT3	Q79ft3 mycobacteri
94	171	19.6	667	2	CAE55351	CAE55351 mycobacte
95	171	19.6	671	2	Q7U0R1	Q7u0r1 mycobacteri
96	170.5	19.6	284	2	Q9BIS8	Q9bis8 tetragantha
97	170.5	19.6	603	1	PG24_MYCTU	O10637 mycobacteri
98	170.5	19.6	615	2	Q7TXQ0	Q7txq0 mycobacteri
99	170.5	19.6	615	2	Q6MX26	Q6mx26 mycobacteri
100	170.5	19.6	615	2	CAE55525	CAE55525 mycobacte

ALIGNMENTS

### RESULT 3

```

RESULT 1
Q14234
ID Q14234 PRELIMINARY; PRT; 757 AA.
AC Q14234;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.,
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA."
RT Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Ala repetitive sequences and few coding sequences."
RL Connect. Tissue Res. 16:197-211(1987).
DR EMBL; M17282; AAC98395.1; -.
DR EMBL; M15983; AAC98395.1; JOINED.
DR EMBL; M17265; AAC98395.1; JOINED.
DR EMBL; M17266; AAC98395.1; JOINED.
DR EMBL; M17267; AAC98395.1; JOINED.
DR EMBL; M17268; AAC98395.1; JOINED.
DR EMBL; M17270; AAC98395.1; JOINED.
DR EMBL; M17271; AAC98395.1; JOINED.
DR EMBL; M17272; AAC98395.1; JOINED.
DR EMBL; M17273; AAC98395.1; JOINED.
DR EMBL; M17274; AAC98395.1; JOINED.
DR EMBL; M17275; AAC98395.1; JOINED.
DR EMBL; M17276; AAC98395.1; JOINED.
DR EMBL; M17277; AAC98395.1; JOINED.
DR EMBL; M17278; AAC98395.1; JOINED.
DR EMBL; M17279; AAC98395.1; JOINED.
DR EMBL; M17280; AAC98395.1; JOINED.
DR EMBL; M17281; AAC98395.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; NAS.
DR GO; GO:0030023; F:extracellular matrix constituent conferring. .; NAS.
DR InterPro; IPR001451; Hexapep transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN
DR PROSITE; PS00100; HEXAPEP_TRANSFEROSES; UNKNOWN 1.
SQ SEQUENCE 757 AA; 66136 MW; 23E7FE5B8AF85C8A_CRC64;

Query Match 100.0%; Score 872; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 5.9e-41;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GVRSLSPELREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGALGVG 60
Db 587 GVRSLSPELREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGALGVG 646
Qy 61 IPGGVVGAGPAAAAAAXAAAKAAQAGLVGAAGLGGVGLGVPGVGGIIPPA 120
Db 647 IPGGVVGAGPAAAAAAXAAAKAAQAGLVGAAGLGGVGLGVPGVGGIIPPA 706
Qy 121 AAKYGAAGLGGVGGAGQFPLGGVAAPQFGLSPIFFPGGACLGKACGRKK 171
Db 707 AAKYGAAGLGGVGGAGQFPLGGVAAPQFGLSPIFFPGGACLGKACGRKK 757

```



707 AAKYGAAGLGGVLGGAGQFLPGVAAAPGFGLSPIFFGACGLGKACGRKRK 757

DB

RESULT 4

Q9UMF5 PRELIMINARY; PRT; 258 AA.

ID Q9UMF5 AC Q9UMF5

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Elastin (Fragment).

GN Name=ELN;

OS Homo sapiens (Human).

OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96411691; PubMed=88124620;

RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,

RA Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,

RA Koop B.F., Tsui L.-C.;

RT "Identification of genes from a 500-kb region at 7q11.23 that is

RT commonly deleted in Williams syndrome patients.";

RL Genomics 36:328-336(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=20458868; PubMed=11003705;

RA Martindale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,

RA Duronio V., Koop B.F.;

RT "Comparative genomic sequence analysis of the Williams syndrome region

RT (11MK1-RPC2) of human chromosome 7q11.23.";

RL Mamm. Genome 11:890-898(2000).

RL EMBL; U63721; AAC13884.1; -.

DR InterPro; IPR001451; Hexapen transf.

DR PROSITE; PS00101; HEXAPEP\_TRANSFERRASES; UNKNOWN\_1.

FT NON\_TER 1

SQ SEQUENCE 258 AA; 21990 MW; C39BF7298D0E05D2 CRC64;

Query Match 83.1%; Score 725; DB 2; Length 258;

Best Local Similarity 97.3%; Pred. No. 4e-33;

Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 25 PPSRPVPGALAAKAAKAAKYGAAVPGVLGGALGGVGFPGVGGAGPAAAAKAAKAA 84

Db 112 PGFGAVPGALAAKAAKAAKYGAAVPGVLGGALGGVGFPGVGGAGPAAAAKAAKAA 171

QY 85 QFLGVCAAGLGGVLGGVGVPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 144

Db 172 QFLGVCAAGLGGVLGGVGVPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 171

QY 145 AARPFGFLSPIPPGGACGLGKACGRKRK 171

Db 232 AARPFGFLSPIPPGGACGLGKACGRKRK 258

ELS HUMAN

ID ELS HUMAN STANDARD; PRT; 730 AA.

AC P15502; Q14233; Q14238;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 05-JUL-2004 (Rel. 14, Last annotation update)

DE Elastin precursor (Tropoelastin).

GN Name=ELN;

OS Homo sapiens (Human).

OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM B).

RA MEDLINE=87289668; PubMed=3039501;

RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,

RA	Rosenbloom J.C., Peltonen L., Rosenbloom J.;	CC	developmental disorder and a contiguous gene deletion syndrome
RT	"Alternative splicing of human elastin mRNA indicated by sequence	CC	involving genes from chromosome band 7q11.23.
RT	analysis of cloned genomic and complementary DNA.";	CC	DISEASE: Defects in ELN are the cause of supravalvular aortic
RL	Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).	CC	stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of
RN	[2]	CC	the ascending aorta which can occur sporadically, as an autosomal
RP	SEQUENCE FROM N.A. (ISOFORM 1).	CC	dominant condition, or as one component of Williams-Beuren
RC	TISSUE=Skin fibroblast;	CC	syndrome.
RX	MEDLINE=89009960; PubMed=3171221;	CC	
RA	Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RA	Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RT	"Cloning of full-length elastin cDNAs from a human skin fibroblast	CC	the European Bioinformatics Institute. There are no restrictions on its
RT	recombinant cDNA library: further elucidation of alternative splicing	CC	use by non-profit institutions as long as its content is in no way
RT	utilizing exon-specific oligonucleotides.";	CC	modified and this statement is not removed. Usage by and for commercial
RL	J. Invest. Dermatol. 91:458-464(1988).	CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
RN	[3]	CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
RP	SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).	CC	
RC	TISSUE=Placenta;	CC	
RX	MEDLINE=88156138; PubMed=2831431;	DR	EMBL; M17282; AAC98394.1; JOINED.
RA	Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,	DR	EMBL; M16983; AAC98394.1; JOINED.
RA	Rosenbloom J., Uitto J.;	DR	EMBL; M17265; AAC98394.1; JOINED.
RT	"Isolation and characterization of human elastin cDNAs, and age-	DR	EMBL; M17266; AAC98394.1; JOINED.
RT	associated variation in elastin gene expression in cultured skin	DR	EMBL; M17267; AAC98394.1; JOINED.
RT	fibroblasts.";	DR	EMBL; M17268; AAC98394.1; JOINED.
RL	Lab. Invest. 58:270-277(1988).	DR	EMBL; M17270; AAC98394.1; JOINED.
RN	[4]	DR	EMBL; M17271; AAC98394.1; JOINED.
RP	SEQUENCE OF 603-730 FROM N.A.	DR	EMBL; M17272; AAC98394.1; JOINED.
RC	TISSUE=Hippocampus, and Placenta;	DR	EMBL; M17273; AAC98394.1; JOINED.
RX	MEDLINE=96291399; PubMed=8689688;	DR	EMBL; M17275; AAC98394.1; JOINED.
RA	Frangiskakis J.M., Ewart A.K., Morris C.B., Bertrand J.,	DR	EMBL; M17276; AAC98394.1; JOINED.
RA	Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,	DR	EMBL; M17277; AAC98394.1; JOINED.
RA	Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,	DR	EMBL; M17278; AAC98394.1; JOINED.
RA	Keating M.T.;	DR	EMBL; M17279; AAC98394.1; JOINED.
RT	"LIM-kinase1 hemizyosity implicated in impaired visuospatial	DR	EMBL; M17280; AAC98394.1; JOINED.
RT	constructive cognition.";	DR	EMBL; M17281; AAC98394.1; JOINED.
RL	Cell 86:59-69(1996).	DR	EMBL; M36860; AAA5382.1; -
RN	[5]	DR	EMBL; M24782; AAA53190.1; -
RP	INVOLVEMENT IN CUTIS LAXA.	DR	EMBL; U62292; AAB17544.1; -
RX	MEDLINE=99091639; PubMed=9873040;	DR	EMBL; X15603; CAA33627.1; -
RA	Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;	DR	PUR; A32707; EAHU.
RA	"Cutis laxa arising from frameshift mutations in exon 30 of the	DR	HSP; P50099; IZFU.
RT	elastin gene (ELN).";	DR	Genew; HGNC:3327; ELN.
RL	J. Biol. Chem. 274:981-986(1999).	DR	MIM; 130160; -
RN	[6]	DR	MIM; 123700; -
RP	INVOLVEMENT IN SVAS.	DR	MIM; 194050; -
RX	PubMed=10942104;	DR	MIM; 185500; -
RA	Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,	DR	GO; GO:0005578; C:extracellular matrix; TAS.
RA	Munnich A., Byskens B., Gewillig M., Devriendt K., Boyd C.D.;	DR	GO; GO:0005615; C:extracellular matrix structural constituent; TAS.
RT	"Isolated supravalvular aortic stenosis: functional haploinsufficiency	DR	GO; GO:0005201; P:cell proliferation; TAS.
RT	of the elastin gene as a result of nonsense-mediated decay.";	DR	GO; GO:0008283; P:cell proliferation; TAS.
RL	Hum. Genet. 106:577-588(2000).	DR	GO; GO:0008015; P:circulation; TAS.
CC	-!- FUNCTION: Major structural protein of tissues such as aorta and	DR	GO; GO:0009887; P:organogenesis; TAS.
CC	nuchal ligament, which must expand rapidly and recover completely.	DR	GO; GO:0007585; P:respiratory gaseous exchange; TAS.
CC	-!- SUBUNIT: The polymeric elastin chains are cross-linked together	DR	InterPro; IPR003978; tropoelastin.
CC	into an extensible 3D network.	DR	PRINTS; PR01500; TROPOLASTIN.
CC	-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.	DR	Alternative splicing; Connective tissue; Repeat; Signal;
CC	-!- EVENT=Alternative splicing; Named isoforms=2;	DR	Structural protein; Williams-Beuren syndrome.
CC	Comment=Additional isoforms seem to exist;	FT	CHAIN 1 26 Elastin.
CC	Name=1;	FT	DISULFID 27 730 By similarity.
CC	Isoid=PI15502-1; Sequence=Displayed;	FT	VARSPPLIC 472 477 Missing (in isoform 2).
CC	Name=2;	FT	/FTId=VSP_004243.
CC	Isoid=PI15502-2; Sequence=VSP_004243;	SQ	SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;
CC	-!- PTM: The crosslinks are made of deaminated Lys.		
CC	-!- DISEASE: Defects in ELN are a cause of autosomal dominant cutis	Query Match	83.1%; Score 725; DB 1; Length 730;
CC	laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder	Best Local Similarity	97.3%; Pred. No. 8.2e-33;
CC	characterized by loose, hyperextensible skin with decreased	Matches 143; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
CC	resilience and elasticity leading to a premature aged appearance.		
CC	The skin changes are often accompanied by extracutaneous	QY	25 PSSPRVFCALAAAKAAYGAAVPGVGLGALGGVIGIPGGVVGAGPAAAAAKAAKAA 84
CC	manifestations, including pulmonary emphysema, bladder	Db	594 EFGAVPGALAAAKAAYGAAVPGVGLGALGGVIGIPGGVVGAGPAAAAAKAAKAA 643
CC	diverticula, pulmonary artery stenosis and pyloric stenosis.	QY	85 QFGLVGAAGLGLGGVGLGGVPGVGGIGIPPAARAAKAYGAAGLGGVVGAGQPLGGV 144
CC	-!- DISEASE: Haploinsufficiency of ELN may be the cause of certain	Db	644 QFGLVGAAGLGLGGVGLGGVPGVGGIGIPPAARAAKAYGAAGLGGVVGAGQPLGGV 703
CC	cardiovascular and musculo-skeletal abnormalities observed in		
CC	Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare		

ID	Q6P0L4	PRELIMINARY;	PRT;	658 AA.
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AC Q6POL4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ELN protein.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL: BC065566; AAH65566.1; -
DR EMBL; BC065566; AAH65566.1; -
SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 70.2%; Score 612; DB 2; Length 658;
Best Local Similarity 85.0%; Pred. No. 1.4e-26;
Matches 125; Conservative 0; Mismatches 4; Indels 18; Gaps 1;

Qy 25 PSSRPVPGALAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 84
Db 530 PGFRAVPFGALAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 589
Qy 85 QFGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 144
Db 590 QFGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 631
Qy 145 AARPGFGLSPIFFPGGACLGKACGRKK 171
Db 632 AARPGFGLSPIFFPGGACLGKACGRKK 658

RESULT 11
Q14235 PRELIMINARY; PRT; 687 AA.
ID Q14235
AC Q14235;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
RL analysis of cloned genomic and complementary DNA.";
RN Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
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Mon Nov 22 12:42:45 2004

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DR GO:0005578; C:extracellular matrix; IEA.
DR GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; Tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 810 AA; 67204 MW; 1ED61ED5AD4F40A2 CRC64;

Query Match 56.1%; Score 489.5; DB 2; Length 810;
Best Local Similarity 55.4%; Pred. No. 1e-19;
Matches 112; Conservative 8; Mismatches 21; Indels 61; Gaps 5;

QY 30 VFGALAAAKAAKYGAA-----VPGVLGGGLGAGVGIPGGVVGAG-PAATAAAAK 78
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 610 VFGSLAAAKAAKYGAAGLGGPGGLGGPGGLGGAGVPGRVAGAAPPAAAAAAAK 669
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 79 AAKAAQFGLVGAAGL-----GGLGVGGLGVPGVGGGLGIPPA 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 670 AAKAAQYGLGGAGGLGAGGLGAGGLGAGGLGAGGLGAGGLGAGGLGAGGLGAGGVSFA 729
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 AAKAAKYGAAGLGGVGGAGOPPLGGVAARPFGLSPIFF----- 157
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 730 AAKAAKYGAAGLGGVL-GARFPFGVVAARPFGLSPIYPGGAGGLGVGGKPKPYG 788
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 158 -----GGACLGKACGRKK 171
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 789 ALGALGYGGGCGFKSCGRKK 810
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 16
ELS MOUSE STANDARD; PRT; 860 AA.
AC P54320;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=Eln;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Lung;
RX MEDLINE=95130069; PubMed=7829060;
RA Wyder K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
RT "Use of an intron polymorphism to localize the tropoelastin gene to
RT mouse chromosome 5 in a region of linkage conservation with human
RT chromosome 7.";
RL Genomics 23:125-131(1994).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- PTM: The crosslinks are made of deaminated Lys.
CC -----
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CC -----
CC EMBL; U08210; AAA80155.1; -.
CC PIR; A55721; EAMS.
CC MGD; MGI:95317; Eln.
CC InterPro; IPR003979; tropoelastin.
CC PRINTS; PR01500; TROPOELASTIN.
CC Connective tissue; Repeat; Signal; Structural protein.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 860 Elastin.

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RA	Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,					
RA	Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;					
RT	"Sequence variation of bovine elastin mRNA due to alternative					
RT	splicing.";					
RL	Coll. Relat. Res. 7:235-247(1987).					
DR	EMBL; M19372; AAA30500.1;					
DR	EMBL; M11422; AAA30500.1; JOINED.					
DR	EMBL; M19366; AAA30500.1; JOINED.					
DR	EMBL; M19367; AAA30500.1; JOINED.					
DR	EMBL; M19368; AAA30500.1; JOINED.					
DR	EMBL; M19369; AAA30500.1; JOINED.					
DR	EMBL; M19370; AAA30500.1; JOINED.					
DR	EMBL; M19371; AAA30500.1; JOINED.					
DR	EMBL; M22771; AAA30500.1; JOINED.					
DR	EMBL; M22772; AAA30500.1; JOINED.					
DR	EMBL; M22773; AAA30500.1; JOINED.					
DR	EMBL; M22774; AAA30500.1; JOINED.					
DR	EMBL; M22988; AAA30500.1; JOINED.					
DR	GO; GO:0005578; C:extracellular matrix; IEA.					
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.					
DR	InterPro; IPR003979; tropoelastin.					
DR	PRINTS; PR01500; TROP0ELASTIN.					
DR	NON_TER	1				
FT	SEQUENCE	679 AA;	57652 MW;	EB3C019E3BD7618D CRC64;		
Query Match 50.7%; Score 442; DB 2; Length 679;						
Best Local Similarity 64.1%; Pred. No. 4e-17;						
Matches 100; Conservative 7; Mismatches 31; Indels 18; Gaps 5;						
Qy	30	VPGLAALAAKAAKYGAAPVGV--LGGI-GALGGVGPVGGVWGNPAAAKAAKAAKAAQFG 87				
Db	528	VEGLGVGAGVPGFPGAGVGGVGLGVGDLGGAGTGGVAGVGP-AAAAAKAAKAAKAAQFG 586				
Qy	88	LVGAAGLGGVGGVGLG-VPGVGGGLGIPPAAAKAAKYGAAGLGGVGLGGAGQFPLGGVAA 146				
Db	587	L---GGVGLGVGGVGLGAVPGVGLGVSPAAAKAAKFAAGLGGVGLGGAGQFPLGGGAG 643				
Qy	147	RPFGGLSPI-----FPGGACLGKACGRKK 171				
Db	644	GLGVGGKPPKPPFGGALGALGFPFGGACLGKSCGRKK 679				
RESULT 22						
Q28099						
ID	Q28099	PRELIMINARY;	PRT;	650 AA.		
AC	Q28099;					
DT	01-NOV-1996	(TrEMBLrel. 01, Created)				
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)				
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)				
DE	Elastin-cBEL1;	NCBI gi: 163003 (Fragment).				
OS	Bos taurus	(Bovine).				
OC	Eukaryota;	Metazoa;	Chordata;	Craniata;	Vertebrata;	Euteleostomi;
OC	Mammalia;	Eutheria;	Cetartiodactyla;	Ruminantia;	Pecora;	Bovidae;
OC	Bovinae;	Bos.				
OX	NCBI_TaxID=9913;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE=85280426;	PubMed=2992576;				
RA	Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,					
RA	Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;					
RT	"Structure of the 3' portion of the bovine elastin gene.";					
RL	Biochemistry 24:3075-3080(1985).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE=88028442;	PubMed=3665402;				
RA	Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,					
RA	Cicila G., May M., Ornstein-Goldstein N., Indik Z., Sheppard P.,					
RA	Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;					
RT	"Sequence variation of bovine elastin mRNA due to alternative					
RT	splicing.";					
RL	Coll. Relat. Res. 7:235-247(1987).					
DR	EMBL; M19372; AAA30499.1;					
DR	EMBL; M11422; AAA30499.1; JOINED.					
DR	EMBL; M19366; AAA30499.1; JOINED.					

SIGNAL	1	26				
CHAIN	27	747	Elastin.			
DISULFID	737	742				
MOD_RES	105	105	Allysine.			
MOD_RES	109	109	Allysine.			
MOD_RES	252	252	Allysine.			
MOD_RES	271	271	Allysine.			
MOD_RES	275	275	Allysine.			
MOD_RES	324	324	Allysine.			
MOD_RES	327	327	Allysine.			
MOD_RES	400	400	Allysine.			
MOD_RES	404	404	Allysine.			
MOD_RES	407	407	Allysine.			
MOD_RES	448	448	Allysine.			
MOD_RES	489	489	Allysine.			
MOD_RES	493	493	Allysine.			
MOD_RES	544	544	Allysine.			
MOD_RES	548	548	Allysine.			
MOD_RES	552	552	Allysine.			
MOD_RES	606	606	Allysine.			
MOD_RES	609	609	Allysine.			
MOD_RES	645	645	Allysine.			
MOD_RES	649	649	Allysine.			
MOD_RES	685	685	Allysine.			
MOD_RES	688	688	Allysine.			
VARSPLOC	226	239	Missing (in isoform 2).			
			/FTid=VSP_004239.			
			Missing (in isoform 3).			
			/FTid=VSP_004240.			
CONFLICT	1	3	MRS -> MAG (in Ref. 2 and 3).			
CONFLICT	12	12	E -> G (in Ref. 2 and 3).			
SEQUENCE	747 AA;	64229 MW;	633C03E411643D83 CRC64;			
Query Match 54.7%; Score 477; DB 1; Length 747;						
Best Local Similarity 66.0%; Pred. No. 4.8e-19;						
Matches 105; Conservative 7; Mismatches 31; Indels 16; Gaps 4;						
Y	25	PSSEPRVPGALAAKAAKYGAAPVGLGGLGALGVGIPGGVWGNPAAAKAAKAAKAA 84				
b	593	PGFGAVPTGLAAAKAAYGFGPGVGLGVGDLGGAG:PGGVAGVVP-AAAAAKAAKAA 651				
Y	85	QFGLVGAAGLGGVGGVGLG-VPGVGGGLGIPPAAAKAAKYGAAGLGGVGLGGAGQFPLGG 143				
b	652	QFGL---GGVGLGVGGVGLGAVPGVGLGVSPAAAKAAKFAAGLGGVGLGGAGQFPLGG 708				
Y	144	VAARPGFGLSPI-----FPGGACLGKACGRKK 171				
b	709	GAGGLGVGGKPPKPPFGGALGALGFPFGGACLGKSCGRKK 747				
RESULT 21						
Q28097						
ID	Q28097	PRELIMINARY;	PRT;	679 AA.		
AC	Q28097;					
DT	01-NOV-1996	(TrEMBLrel. 01, Created)				
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)				
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)				
DE	Elastin-cBEL2;	NCBI gi: 163004 (Fragment).				
OS	Bos taurus	(Bovine).				
OC	Eukaryota;	Metazoa;	Chordata;	Craniata;	Vertebrata;	Euteleostomi;
OC	Mammalia;	Eutheria;	Cetartiodactyla;	Ruminantia;	Pecora;	Bovidae;
OC	Bovinae;	Bos.				
OX	NCBI_TaxID=9913;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE=85280426;	PubMed=2992576;				
RA	Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,					
RA	Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;					
RT	"Structure of the 3' portion of the bovine elastin gene.";					
RL	Biochemistry 24:3075-3080(1985).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE=88028442;	PubMed=3665402;				
EX						



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EMBL; M26188; AAA31515.1; ALT\_SEQ.  
EMBL; M26189; AAA31516.1; -.  
PIR; S59623; S59623.  
Connective tissue; Repeat; Structural protein.  
NON\_TER 1  
DISULFID 90 95 By similarity.  
SEQUENCE 100 AA; 8662 MW; 5C680C6A5AE86786 CRC64;

Query Match 33.9%; Score 295.5; DB 1; Length 750;  
Best Local Similarity 28.7%; Pred. No. 5.7e-09;  
Matches 102; Conservative 12; Mismatches 33; Indels 209; Gaps 12;

QY 21 LPTSSSRVPG-----ALAAKAAKYGA-----AVPGVLGGLGALG-- 57  
Db 399 VFGVGVPGVGPGVGGVGPAAAAAKAAAFAGAGRPVGVGVGVPVGVGVG 458  
QY 58 -----GVGIPGGVGVGAPAAAATAAKAA 80  
Db 459 VFGVGVPGVGPGVGVGPGVGVGPGVGVGPGVGVGPGVGVGPGVGVGPG 515  
QY 81 AKAAQFGLVG-----AAGLGLL---GVGGLGVPGVGGGL---GGIPPA--- 116  
Db 516 AKAAKYAGGLAPGVGLIAPAVGGLIAPGVGLIAPGVGLIAPGVGLIAPGV 574  
QY 117 -----AAKAAKYGAA-----GLGGV----- 132  
Db 575 VFGVGSPAAAAAKAAAKYAGVGVPVGVGPGVGVGPGVGVGPGVGVGPGV 634  
QY 133 -----LGACAGFPPLGGV 144  
Db 635 PGVGVLPAGIFPVGVQPGAKPKTFPGVPGVGVGPGVGVGPGVGVGPGVGV 694  
QY 145 AARPFGGLSPIPFG-----GACLGKACGRKK 171  
Db 695 VGVPGVSPFPPGVGGVGGQLGFGKPKTYGGALGALGFRGGVGCAGKYCG 750

RESULT 24  
ELS\_SHEEP STANDARD; PRT; 100 AA.

AC P11547; (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
EL Elastin (Tropoelastin) (Fragment).  
GN Name=ELN;  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Ovis.  
NCBI\_TaxID=9940;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=85305763; PubMed=3839997;  
RA Yoon K., Davidson J.M., Boyd C., May M., Luvalle P., Smith E.,  
RA Ornstein-Goldstein N., Smith J.J., Indik Z., Ross A., Golub E.,  
RA Rosenbloom J.;  
RT Arch. Biochem. Biophys. 241:684-691(1985).  
CC -|- FUNCTION: Major structural protein of tissues such as aorta and  
CC nuchal ligament, which must expand rapidly and recover completely.  
CC -|- SUBUNIT: The polymeric elastin chains are cross-linked together  
CC into an extensible 3D network.  
CC -|- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.  
CC -|- PTM: The crosslinks are made of deaminated lys.  
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231 SPEAQAATAAATAAAGTGLVPGVGVAGVPGVAGVPGVAGVPGVGLAP--GVGVAPGVGVAPGVG 28

QY 155 ----IFPGG-ACLGKACGR 168  
 Db 289 VAPGIGPGVGAATAAASAAK 307

RESULT 26  
 O15337 PRELIMINARY; PRT; 602 AA.

ID O15337  
 AC O15337;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Elastin (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97358574; PubMed=9215670;  
 RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,  
 RA Morris C.A., Keating M.T.;  
 RT "Elastin point mutations cause an obstructive vascular disease,  
 RT supravalvular aortic stenosis.";  
 RL Hum. Mol. Genet. 6:1021-1028(1997).  
 DR EMBL; U93037; AAB65620.1; -.  
 DR EMBL; U93034; AAB65620.1; JOINED.  
 DR EMBL; U93035; AAB65620.1; JOINED.  
 DR EMBL; U93036; AAB65620.1; JOINED.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
 DR InterPro; IPR001451; Hexapep transf.  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOELASTIN.  
 DR PROSITE; PS00101; HEXAPEP\_TRANSFEROSES; UNKNOWN\_1.  
 FT NON\_TER 1  
 FT NON\_TER 602  
 SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 31.4%; Score 273.5; DB 2; Length 602;  
 Best Local Similarity 36.6%; Pred. No. 8.2e-08;  
 Matches 94; Conservative 13; Mismatches 29; Indels 121; Gaps 14;

QY 28 PRVPGAL-----AAAKAAKYGAAV-----PGVLGGGLGA-LG 57  
 Db 255 PGVPGAIPGIGIAGVGTAAAAAATAAATAAAGTVPVGGPGVGVPGAGVP 314  
 QY 58 GVGIPIGG-----VVGAG-PAAAA-----AAKAAKAAQAQGL-----VGAA 92  
 Db 315 GVGVPGAGIPVPGAGIPGAAPGVGWSPEAAKAAKAAKAAKYGARPGVGVGPIYGVGAG 374  
 QY 93 GLGGLGVGLGVPGVG-----GLGGIP-----PAAAKAAKYGAGLGGVIG 134  
 Db 375 GFPGFGVGVGIPGVAGVPSVGGVPGVGVGPGVGISPEAATAAATAAATAAAG-AGVLG 433  
 QY 135 G-----AGQFPL-----GGVAARPPGGLS 153  
 Db 434 GLVPGAAGVPGVPGTGVPGVGTAAAAAATAAATAAAGTLLAGLVPGVGVAGVGVGA 493

QY 154 P----IFPGGACLGKACG 167  
 Db 494 PGVGVAPG---VGLAPG 507

RESULT 27  
 O15336 PRELIMINARY; PRT; 635 AA.

ID O15336  
 AC O15336;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE	Elastin (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97358574; PubMed=9215670;
RA	Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA	Morris C.A., Keating M.T.;
RT	"Elastin point mutations cause an obstructive vascular disease,
RT	supraaortic valvular aortic stenosis."
RL	Hum. Mol. Genet. 6:1021-1028(1997).
DR	EMBL; U930337; AAB65621.1; .
DR	EMBL; U930334; AAB65621.1; JOINED.
DR	EMBL; U93035; AAB65621.1; JOINED.
DR	EMBL; U93036; AAB65621.1; JOINED.
DR	GO; GO:0005578; C:extracellular matrix; IEA.
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR	InterPro; IPR001451; Hexapep transf.
DR	InterPro; IPR003979; tropoelastin.
DR	PRINTS; PR01500; TROP0ELASTIN.
DR	PROSITE; PS00101; HEXAPEP_TRANSFEROSES; UNKNOWN_1.
FT	NON TER 1
FT	NON TER 635
SQ	SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;

  

Query Match	31.4%; Score 273.5; DB 2; Length 635;
Best Local Similarity	36.6%; Pred.No. 8.5e-08;
Matches	94; Conservative 13; Mismatches 29; Indels 121; Gaps 14;

  

Qy	28	PRVPGAL-----AAKAAKYGRAV-----PPVLGGLGA-LG 57
Dd	255	PGVPEALPGTGGIAGVTTPAAAAAAXKAYGAAAGLVPGPGPGWVGVPAGVP 314
Qy	58	GVGIPGG----VVGAG-PAAAA-----AAKAAAKAAQFGL-----VGAA 92
Dd	315	GVGVPGAGIPVPGAGIPGAAPGVVSPEAAAAXKAAKGARPGVGVGGIPTYGVGAG 374
Qy	93	GLGLGVGGLGVPGVG-----GLGGIP-----PAAAAAAXKAYGAAAGLGGVLG 134
Dd	375	GFFPGFGVGVGGIPGVAGVPSGVGVGVGGISPEAQAAAAAAXKAYGAAG-AGVLG 433
Qy	135	G-----AGQPPL-----GGVAARPQGFLS 153
Dd	434	GLVPGAPGAVPVGPVGTTPAAAAAAXKAAAFALLNLGLVGVGVAPGVGVA 493
Qy	154	P---IFPGGACLGKACG 167
Dd	494	PGVGVAPG---VGLAPG 507

  

RESULT 28
Q6ZUN2
ID Q6ZUN2 PRELIMINARY; PRT; 559 AA.
AC Q6ZUN2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43523.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saïto K., Nishikawa T., Kimura K., Yamashita H.,
PA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
PA Murakawa Y., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,

RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK125511; BAC86188.1; --  
 DR InterPro; IPR003979; tropoelastin.  
 DR PRINTS; PR01500; TROPOLASTIN.  
 SQ SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 30.8%; Score 269; DB 2; Length 559;  
 Best Local Similarity 42.0%; Pred. No. 1.4e-07;  
 Matches 84; Conservative 12; Mismatches 40; Indels 64; Gaps 11;

QY 24 TPSPRPVPGALAAAKAAKYCAAVPVGLGLGALGVGIP-----GGWVGAGPAAAAAA 77  
 DB 243 TGVGPQAAAAAAAKAAKAFGAGAAGVLPVGGGAGVPGVPAIPGIGIAGVGTPTAAAAA 302

QY 78 KAAAKAAQFGLVGAAGL-----GGLGVGGLGVPGVG--GLG-----GIPPA--- 116  
 DB 303 AAAAKAAKYG--AAAGLVPGGPGFGVGVPGAGVPGVPGAGIPVVPVPGAGIPGAAPV 360

QY 117 -----AAAKAAKYGA---AGLGGV--LG-GAGQFP-----LGVVAARPFGFL 152  
 DB 361 GVVSPEAAAKAAAKAAYGARPGVGGIPTYGVGAGGFGFGVGGVGGIPGVAGVPGVGG 420

QY 153 S-----PIFFPGAC 161  
 DB 421 SRSRRCPGSHWFFRSGSSC 440

RESULT 29  
 BAC86188 PRELIMINARY; PRT; 559 AA.

ID BAC86188  
 AC BAC86188;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CNA FLJ43523 fis, clone PLAC5000282, weakly similar to Homo sapiens elastin (supraaavalvular aortic stenosis, Williams-Beuren syndrome) (ELN).  
 DE Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RS SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Arita M., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Oshima A., Takashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK125511; BAC86188.1; --  
 SQ SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 30.8%; Score 269; DB 2; Length 559;  
 Best Local Similarity 42.0%; Pred. No. 1.4e-07;  
 Matches 84; Conservative 12; Mismatches 40; Indels 64; Gaps 11;

QY 24 TPSPRPVPGALAAAKAAKYCAAVPVGLGLGALGVGIP-----GGWVGAGPAAAAAA 77  
 DB 243 TGVGPQAAAAAAAKAAKAFGAGAAGVLPVGGGAGVPGVPAIPGIGIAGVGTPTAAAAA 302

QY 78 KAAAKAAQFGLVGAAGL-----GGLGVGGLGVPGVG--GLG-----GIPPA--- 116  
 DB 303 AAAAKAAKYG--AAAGLVPGGPGFGVGVPGAGVPGVPGAGIPVVPVPGAGIPGAAPV 360

QY 117 -----AAAKAAKYGA---AGLGGV--LG-GAGQFP-----LGVVAARPFGFL 152  
 DB 361 GVVSPEAAAKAAAKAAYGARPGVGGIPTYGVGAGGFGFGVGGVGGIPGVAGVPGVGG 420

QY 153 S-----PIFFPGAC 161  
 DB 421 SRSRRCPGSHWFFRSGSSC 440

RESULT 30  
 O9GUB5 PRELIMINARY; PRT; 1468 AA.

ID O9GUB5  
 AC O9GUB5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Heavy-chain fibroin (Fragment).  
 GN Name-Fib-H;  
 OS Galleria mellonella (Wax moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;  
 OC Pyralidae; Galleriinae; Galleria.  
 OX NCBI\_TaxID=7137;  
 RN [1]  
 RS SEQUENCE FROM N.A.  
 RC TISSUE=Posterior silk gland;  
 RX MEDLINE=22063245; PubMed=11886872;  
 RA Zurovec M., Sehna F.;  
 RT "Unique molecular architecture of silk fibroin in the waxmoth, Galleria mellonella."  
 RL J. Biol. Chem. 277:22639-22647(2002).  
 DR EMBL; AF095239; AAG10393.1; --  
 FT NONTER 1468 1468  
 SQ SEQUENCE 1468 AA; 122704 MW; 2DA59E1181BB3DDF CRC64;

Query Match 24.5%; Score 213.5; DB 2; Length 1468;  
 Best Local Similarity 39.1%; Pred. No. 0.00033;  
 Matches 63; Conservative 17; Mismatches 42; Indels 39; Gaps 6;

QY 32 GALAAAKAAKYCAAVPVG---LGLGALGVGIPG-----GVVVGAGPAAAAAAKA 79  
 DB 351 GPIGATSASTGAGLGVGAAGAGSLGLGAGASAGAGLGGIGAGGSSGSSAASA 410

QY 80 AAKAAQFGLV-----GAGLGLGVGGLGVPGVPGVGGIPPPAAAAKAA 122  
 DB 411 ASGASGAGEVIVIDRRSSAASAAASGASGLGLGGLGPGYGGIGLVSSASAL--- 467

QY 123 KYGAAGLGVGAGQFPLGVGAARPGFGLSPIFFPGACLG 163  
 DB 468 ---GAGLGGV-GTAGASLGLG---GAGVSAVGPAGAGLG 501

Search completed: November 19, 2004, 16:36:52  
 Job time : 36.5734 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 37.3991 Seconds  
(without alignments)  
1755.321 Million cell updates/sec

Title: US-09-743-818A-74

Perfect score: 935

Sequence: 1 AAAGLGAGIPGLGVGVGVPQ.....LSPIFGAGLKGACGRKK 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	935	100.0	183	2	Aay01311 Human tro
2	935	100.0	183	3	Aay69138 Amino aci
3	935	100.0	692	7	Ade40134 Human NOV
4	935	100.0	698	2	Aay01302 Human tro
5	935	100.0	698	3	Aay69069 Amino aci
6	935	100.0	730	5	Aao17360 Human ela
7	935	100.0	730	8	AQD19747 Human sof
8	927	99.1	663	7	Adm03792 Human pro
9	920.5	98.4	660	2	Aay01303 Human tro
10	908.5	97.2	216	2	Aay01310 Human tro
11	908.5	97.2	731	3	Aay69068 Human ela
12	908.5	97.2	731	4	AAB66657 Human ela
13	908.5	97.2	731	6	ABU08725 Human ela
14	908.5	97.2	731	7	ADL96420 Human ela
15	908.5	97.2	733	2	AAR56653 Synthetic
16	908.5	97.2	733	2	Aay01301 Amino aci
17	908.5	97.2	757	7	ABG75223 Human tro
18	908.5	97.2	757	7	ADP65160 Human ela
19	892	95.4	730	2	AAW46315 Human ela
20	822	87.9	617	7	ADB64761 Human pro
21	822	87.9	712	3	AAB08630 Amino aci
22	822	87.9	730	3	AAB08631 Fusion pr
23	819	87.6	711	7	ADE40132 Human NOV
24	801	85.7	200	2	Aay01305 Human tro
25	729	78.0	147	2	Aay01304 Human tro

Accession	Protein	Length (aa)	Score	E-value	Identity (%)	Positives (%)	Gap (%)
Q9	1	AAAGLGGATGTLGVGVGVPGLGVGAGVPGGLGVGAGVPGGAVPGALAAAKAAKAYGAAPVG	60		100	100	0
Db	1	AAAGLGGATGTLGVGVGVPGLGVGAGVPGGLGVGAGVPGGAVPGALAAAKAAKAYGAAPVG	60		100	100	0
Q9	61	VLGGHGLGALGGVGIPEGVVYVAGAPAAAAAKAAAKAAQFGLGVNAGLGGIYGVGSLGVPGVG	120		100	100	0



Db 61 VLGGGLGALGVGIPGGVVGAGPAAAKAAQFGLVGAAGLGGVGLGVPVG 120  
QY 121 GLGGIPPAAKAAKAYGAAGLGGVVGAGQFPLGGVGAARPGFGLSPIFFGGACLGKACGR 180  
Db 121 GLGGIPPAAKAAKAYGAAGLGGVVGAGQFPLGGVGAARPGFGLSPIFFGGACLGKACGR 180  
QY 181 KRK 183  
Db 181 KRK 183

## RESULT 3

ADE40134  
ID ADE40134 standard; protein; 692 AA.

XX AC ADE40134;

DT 29-JAN-2004 (first entry)

DE Human NOV16b protein - SEQ ID 40.

XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
KW anti-diabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
KW anti-parkinsonian; antiasthmatic; gynaecological; cardiomyopathy;  
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
KW tissue typing; human; NOV.

OS Homo sapiens.

XX WO2003064589-A2.

XX 07-AUG-2003.

PF 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

PR 03-AUG-2001; 2001US-0310291P.

PR 07-AUG-2001; 2001US-0310544P.

PR 08-AUG-2001; 2001US-0310951P.

PR 09-AUG-2001; 2001US-0311292P.

PR 13-AUG-2001; 2001US-0311979P.

PR 16-AUG-2001; 2001US-0312892P.

PR 17-AUG-2001; 2001US-0313201P.

PR 20-AUG-2001; 2001US-0313415P.

PR 20-AUG-2001; 2001US-0313643P.

PR 21-AUG-2001; 2001US-0313702P.

PR 21-AUG-2001; 2001US-0314031P.

PR 23-AUG-2001; 2001US-0314466P.

PR 28-AUG-2001; 2001US-0315403P.

PR 29-AUG-2001; 2001US-0315853P.

PR 17-SEP-2001; 2001US-0322716P.

PR 21-SEP-2001; 2001US-0323994P.

PR 14-DEC-2001; 2001US-0340233P.

PR 05-FEB-2002; 2002US-0354591P.

PR 19-MAR-2002; 2002US-0365478P.

PR 19-APR-2002; 2002US-0373814P.

PR 19-APR-2002; 2002US-0373825P.

PR 23-APR-2002; 2002US-0373989P.

PR 07-JUN-2002; 2002US-0374632P.

PR 07-JUN-2002; 2002US-0386971P.

PR 01-AUG-2002; 2002US-00210172.

XX (CURA-) CURAGEN CORP.

PI Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;

PI Shimkets RA, Zerhusen BD, Li L, Ji W, Padigar M,

PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;

PI Guo X, Zhong M, Gerlach VL, Hjalt I, Rastelli L, Spytek KA;

PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;

PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;

PI Smithson G;

XX WPI; 2003-663472/62.

DR N-PSDB; ADE40133.

XX

PT New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.

XX Claim 1; SEQ ID NO 40; 560pp; English.

XX The invention relates to a novel NOVX polypeptide. The polypeptide of the  
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,  
CC cyrostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and  
CC gynaecological activities and may be useful in diagnosing, treating or  
CC preventing NOVX-associated disorders including cardiomyopathy,  
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple  
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
CC be utilised as vaccines whilst the nucleic acids may be used as  
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
CC preventive medicine and pharmacogenomics. The current sequence is that of  
CC the human NOV protein of the invention.

XX Sequence 692 AA;

Query Match 100.0%; Score 935; DB 7; Length 692;

Best Local Similarity 100.0%; Pred. No. 9.9e-58;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGVGAGVPGFAGVPGALAAKAAKYGAAPVG 60

Db 510 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGVGAGVPGFAGVPGALAAKAAKYGAAPVG 569

QY 61 VLGGGLGALGVGIPGGVVGAGPAAAKAAQFGLVGAAGLGGVGLGVPVG 120

Db 570 VLGGGLGALGVGIPGGVVGAGPAAAKAAQFGLVGAAGLGGVGLGVPVG 629

QY 121 GLGGIPPAAKAAKAYGAAGLGGVVGAGQFPLGGVGAARPGFGLSPIFFGGACLGKACGR 180

Db 630 GLGGIPPAAKAAKAYGAAGLGGVVGAGQFPLGGVGAARPGFGLSPIFFGGACLGKACGR 689

QY 181 KRK 183

Db 690 KRK 692

## RESULT 4

AAAY01302

ID AAAY01302 standard; protein; 698 AA.

XX AC AAAY01302;

XX 07-JUN-1999 (first entry)

DE Human tropoelastin variant SHELdelta26A.

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.

OS Homo sapiens.

OS Synthetic.

PN WO9903886-A1.

XX 28-JAN-1999.

XX 17-JUL-1998; 98WO-AU000564.

XX 18-JUL-1997; 97AU-00008117.

XX PA (UNSY ) UNIV SYDNEY.  
XX PI Weiss AS;  
XX DR WPI; 2000-182399/16.  
XX DR N-PSDB; AA261144.  
XX PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
XX PT cell growth.  
XX PS Disclosure; Page 110-112; 136pp; English.  
XX CC The present sequence represents a human reduced tropoelastin derivative,  
XX CC designated SHEL-delta-26a. The sequence is produced by removing exon 26a  
XX CC of SHEL (SHEL not defined). The protein is representative of tropoelastin  
XX CC derivatives of the invention, in which a subsequence has been mutated so  
XX CC that susceptibility to proteolysis is reduced or eliminated, or a  
XX CC subsequence has been inserted so that susceptibility to proteolysis is  
XX CC increased. The derivatives have with reduced susceptibility, and can be  
XX CC used where the wild-type protein would be degraded too easily, e.g. in  
XX CC contact with serum or wound exudate. The tropoelastin derivatives provide  
XX CC competitive inhibition of protease activity. The tropoelastin  
XX CC derivatives, and other polypeptides containing tropoelastin derivative-  
XX CC derived protease-susceptibility sites, are useful in human or veterinary  
XX CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
XX CC and for inducing chemotaxis. They are also useful for proliferation or  
XX CC growth inhibition, particularly of smooth muscle cells, epithelial or  
XX CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
XX CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
XX CC derivatives are competitive inhibitors of the protease, and are used for  
XX CC protecting against lung damage caused by elastin, for inhibiting or  
XX CC controlling localized growth of cancers or metastases, or to limit  
XX CC protease activity that causes blood clotting  
XX SQ Sequence 698 AA;  
Query Match 100.0%; Score 935; DB 3; Length 698;  
Best Local Similarity 100.0%; Pred. No. 1e-57;  
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGVPGALAAAKAAYGAAVPG 60  
DB 516 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGVPGALAAAKAAYGAAVPG 575  
QY 61 VLGGGLGALGGVGPVGGVGGAGPAAAAAATAAQAQFGLVGAAGLGGVGLGVPGVG 120  
DB 576 VLGGGLGALGGVGPVGGVGGAGPAAAAAATAAQAQFGLVGAAGLGGVGLGVPGVG 635  
QY 121 GLGGIPPAATAAKAAYGAAAGLGGVGLGGAGQFPLGGVAARPFGLSPIPPGACLGKACGR 180  
DB 636 GLGGIPPAATAAKAAYGAAAGLGGVGLGGAGQFPLGGVAARPFGLSPIPPGACLGKACGR 695  
QY 181 KRK 183  
DB 696 KRK 698  
RESULT 6  
AAO17360  
ID AAO17360 standard; protein; 730 AA.  
XX AC AAO17360;  
XX DT 19-JUL-2002 (first entry)  
XX DE Human elastin.  
XX KW Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;  
KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;  
KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;  
KW transmembrane receptor PTK7; collagen type XVIII alpha 1;  
KW platelet derived growth factor receptor alpha; laminin M chain;

XX PA (UNSY ) UNIV SYDNEY.  
XX PI Weiss AS;  
XX DR WPI; 1999-132162/11.  
XX PT New derivatives of human tropoelastin - with elastin-like or  
XX PT macromolecular binding properties, useful e.g. as surgical implants.  
XX PS Claim 13; Fig 2; 82pp; English.  
XX CC The invention relates to a derivative or variant of human tropoelastin  
XX CC (hTE) having elastin-like and/or macromolecule (specifically  
XX CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
XX CC comprising the nucleic acids encoding the variants or derivatives are  
XX CC used to produce the proteins recombinantly. The tropoelastin derivatives  
XX CC or hybrid proteins containing the derivatives are useful in medical,  
XX CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
XX CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
XX CC products. The hybrid protein have controllable GAG-binding properties,  
XX CC depending on presence or absence of a specific fragment, designated  
XX CC peptide 26A, from hTE. The present sequence represents the synthetic  
XX CC human tropoelastin variant SHELdelta26A  
XX SQ Sequence 698 AA;  
Query Match 100.0%; Score 935; DB 2; Length 698;  
Best Local Similarity 100.0%; Pred. No. 1e-57;  
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGVPGALAAAKAAYGAAVPG 60  
DB 516 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGVPGALAAAKAAYGAAVPG 575  
QY 61 VLGGGLGALGGVGPVGGVGGAGPAAAAAATAAQAQFGLVGAAGLGGVGLGVPGVG 120  
DB 576 VLGGGLGALGGVGPVGGVGGAGPAAAAAATAAQAQFGLVGAAGLGGVGLGVPGVG 635  
QY 121 GLGGIPPAATAAKAAYGAAAGLGGVGLGGAGQFPLGGVAARPFGLSPIPPGACLGKACGR 180  
DB 636 GLGGIPPAATAAKAAYGAAAGLGGVGLGGAGQFPLGGVAARPFGLSPIPPGACLGKACGR 695  
QY 181 KRK 183  
DB 696 KRK 698  
RESULT 5  
AAAY69069  
ID AAAY69069 standard; protein; 698 AA.  
XX AC AAAY69069;  
XX DT 30-MAY-2000 (first entry)  
XX DE Amino acid sequence of a human reduced tropoelastin derivative.  
XX KW Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease;  
KW antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;  
KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;  
KW metastasis; blood clotting.  
XX OS Synthetic.  
XX OS Homo sapiens.  
XX PN WO200004043-A1.  
XX PD 27-JAN-2000.  
XX XX 19-JUL-1999; 99WO-AU000580.  
XX PF 17-JUL-1998; 98AU-00004723.  
XX PR



DS	Synthetic.
XX	WO9903886-A1.
XX	28-JAN-1999.
XX	17-JUL-1998; 98WO-AU000564.
XX	18-JUL-1997; 97AU-00008117.
XX	(UNSY ) UNIV SYDNEY.
XX	Weiss AS;
XX	WPI; 1999-132162/11.
XX	N-PSDB; AAX27705.
XX	New derivatives of human tropoelastin - with elastin-like or
PPT	macromolecular binding properties, useful e.g. as surgical implants.
PPT	Claim 7; Fig 3; 82pp; English.
XX	The invention relates to a derivative or variant of human tropoelastin
CC	(hTE) having elastin-like and/or macromolecule (specifically
CC	glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC	comprising the nucleic acids encoding the variants or derivatives are
CC	used to produce the proteins recombinantly. The tropoelastin derivatives
CC	or hybrid proteins containing the derivatives are useful in medical,
CC	pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC	wrinkle or hand lotion, also as surgical implants, foods and industrial
CC	products. The hybrid protein have controllable GAG-binding properties,
CC	depending on presence or absence of a specific fragment, designated
CC	peptide 26A, from hTE. The present sequence represents a human
CC	tropoelastin derivative SHELdelta modified
XX	Sequence 660 AA;
SQ	Query Match 98.4%; Score 920.5; DB 2; Length 660;
	Best Local Similarity 99.5%; Pred. No. 9.9e-57; Indels 1; Gaps 1
	Matches 182; Conservative 0; Mismatches 0;
QY	1 AAAGLGAGTGLGVGVPGVLGVGAGVPGFGLGVGAGVPGFAGVPGALAAAKAAYGAVPG 60
Db	479 AAAGLGAGTGLGVGVPGVLGVGAGVPGFGLGVGAGVPGFAGVPGALAAAKAAYG-AVPG 537
QY	61 VLGGGLGALGGVGIPGGVVGAGPAAAAKAAKAAOFGLVGAAGLGSGLGVGGLGVPGVG 120
Db	538 VLGGGLGALGGVGIPGGVVGAGPAAAAKAAKAAOFGLVGAAGLGSGLGVGGLGVPGVG 597
QY	121 GLGGIPPAKAAKAYCAAGLGGVLGGAGOPFLGGVAARPFGLSPIPPGGACLGKACGR 180
Db	598 GLGGIPPAKAAKAYCAAGLGGVLGGAGOPFLGGVAARPFGLSPIPPGGACLGKACGR 657
QY	181 KRK 183
Db	658 KRK 660
RESULT 10	
AAY01310	
ID	AAY01310 standard; protein; 216 AA.
XX	AAY01310;
XX	07-JUN-1999 (first entry)
DT	Human tropoelastin derivative SHEL26-36.
DE	Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW	pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW	hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX	Homo sapiens.
OS	

OS Synthetic.  
 PN WO9903886-A1.  
 XX  
 PD 28-JAN-1999.  
 XX  
 PF 17-JUL-1998; 98WO-AU000564.  
 XX  
 PR 18-JUL-1997; 97AU-00008117.  
 XX  
 PA (UNSY ) UNIV SYDNEY.  
 XX  
 PI Weiss AS;  
 XX  
 DR WPI; 1999-132162/11.  
 XX  
 PT New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.  
 XX  
 PS Claim 35; Page 11; 82pp; English.  
 XX  
 CC The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents a human  
 CC tropoelastin derivative SHEL26-36  
 XX  
 SQ Sequence 216 AA;

Query Match 97.2%; Score 908.5; DB 2; Length 216;  
 Best Local Similarity 84.7%; Pred. No. 2.6e-56;  
 Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

OY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41  
 DB 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41  
 OY 42 -----VPGALAAKAAKYGAAVPGVLGGVPGVLGVGAGVPGFGA----- 41  
 DB 61 SSSQHLPTSPSSPRVPGALAAKAAKYGAAVPGVLGGVPGVLGVGAGVPGFGA----- 41  
 OY 88 AAKAAKAAQFGLVGAAGLGGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41  
 DB 121 AAKAAKAAQFGLVGAAGLGGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41  
 OY 148 AGQPLGGVAARPGLSPFPGGACLGKACGRKK 183  
 DB 181 AGQPLGGVAARPGLSPFPGGACLGKACGRKK 216

RESULT 11  
 AAY69068  
 ID AAY69068 standard; protein; 731 AA.  
 XX  
 AC AAY69068;  
 XX  
 DT 30-MAY-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human tropoelastin splice form.  
 XX  
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX  
 OS Homo sapiens.  
 XX

PH Key Location/Qualifiers  
 FT Cleavage-site 441..442  
 FT Cleavage-site 503..504  
 FT Cleavage-site 515..516  
 FT Cleavage-site 564..565  
 XX WO200004043-A1.  
 XX  
 XX 27-JAN-2000.  
 PD  
 XX 19-JUL-1999; 99WO-AU000580.  
 PF  
 XX 17-JUL-1998; 98AU-00004723.  
 PR  
 XX (UNSY ) UNIV SYDNEY.  
 PA  
 XX Weiss AS;  
 PI  
 XX WPI; 2000-182399/16.  
 DR N-PSDB; AA261146.  
 DR  
 XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 XX cell growth.  
 PT  
 XX Disclosure; Page 107-109; 136pp; English.  
 PS  
 XX The present sequence represents a human tropoelastin splice form. The  
 CC specification describes tropoelastin derivatives, in which a subsequence  
 CC has been mutated so that susceptibility to proteolysis is reduced or  
 CC eliminated, or a subsequence has been inserted so that susceptibility to  
 CC proteolysis is increased. The derivatives have with reduced  
 CC susceptibility, and can be used where the wild-type protein would be  
 CC degraded too easily, e.g. in contact with serum or wound exudate. The  
 CC tropoelastin derivatives provide competitive inhibition of protease  
 CC activity. The tropoelastin derivatives, and other polypeptides containing  
 CC tropoelastin derivative-derived protease-susceptibility sites, are useful  
 CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand  
 CC lotions), as bulking agents and for inducing chemotaxis. They are also  
 CC useful for proliferation or growth inhibition, particularly of smooth  
 CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,  
 CC chondrocytes and platelets. Peptidomimetics that mimic the protease  
 CC cleavage site in tropoelastin derivatives are competitive inhibitors of  
 CC the protease, and are used for protecting against lung damage caused by  
 CC elastin, for inhibiting or controlling localized growth of cancers or  
 CC metastases, or to limit protease activity that causes blood clotting  
 XX  
 SQ Sequence 731 AA;

Query Match 97.2%; Score 908.5; DB 3; Length 731;  
 Best Local Similarity 84.7%; Pred. No. 7.5e-56;  
 Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

OY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41  
 DB 516 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41  
 OY 42 -----VPGALAAKAAKYGAAVPGVLGGVPGVLGVGAGVPGFGA----- 41  
 DB 576 SSSQHLPTSPSSPRVPGALAAKAAKYGAAVPGVLGGVPGVLGVGAGVPGFGA----- 41  
 OY 88 AAKAAKAAQFGLVGAAGLGGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41  
 DB 636 AAKAAKAAQFGLVGAAGLGGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41  
 OY 148 AGQPLGGVAARPGLSPFPGGACLGKACGRKK 183  
 DB 696 AGQPLGGVAARPGLSPFPGGACLGKACGRKK 731

RESULT 12  
 AAB66657  
 ID AAB66657 standard; protein; 731 AA.  
 XX



636 AAKAAKAAQFGLVGAAGLGGVGLGVGVPGLGIPPAKAAKAAKYGAAGLGGVGG 695  
148 AGQFPLGGVAARPGFGLSPFPFGACLGKACGRKK 183  
696 AGQFPLGGVAARPGFGLSPFPFGACLGKACGRKK 731

Db 636 AAKAAKAAQFGLVGAAGLGGVGLGVGVPGLGIPPAKAAKAAKYGAAGLGGVGG 695  
QY 148 AGQFPLGGVAARPGFGLSPFPFGACLGKACGRKK 183  
Db 696 AGQFPLGGVAARPGFGLSPFPFGACLGKACGRKK 731  
RESULT 14  
ADL96420  
ID ADL96420 standard; protein; 731 AA.  
AC ADL96420;  
DT 20-MAY-2004 (first entry)  
XX Human elastin protein fragment.  
DE fibrous protein; prosthesis; elastin; lamprin; spider silk protein;  
KW blood vessel; wound; burn healing; collagen.  
XX Homo sapiens.  
FH Key  
FT Region  
FT /note= "region specifically claimed in claim 6"  
FT 188. .367  
FT /note= "region specifically claimed in claim 6"  
FT 374. .499  
FT /note= "region specifically claimed in claim 6"  
FT 607. .717  
FT /note= "region specifically claimed in claim 6"  
XX US2003166846-A1.

PN 04-SEP-2003.  
PD 28-SEP-2001; 2001US-00964662.  
XX 07-AUG-1996; 96US-0023522P.  
PR 07-AUG-1997; 97US-00911364.  
PR 29-JUN-1999; 99US-00340736.  
XX (ROTH/) ROTHSTEIN A.  
PA (KEEL/) KEELEY F.  
PA (ROTH/) ROTHSTEIN S.  
PI Rothstein A, Keeley F, Rothstein S;  
XX WPI; 2003-898105/82.  
DR Polypeptide for constructing human elastin-like prostheses such as tubes  
XX for blood vessel replacement and sheets for other uses such as wound or  
FT burn healing, comprises three beta sheets and three beta turns.  
XX Claim 5; Fig 1B; 17pp; English.  
XX This invention describes a polypeptide that comprises three beta  
XX sheet/beta turn structures and that is not a naturally occurring fibrous  
XX protein. The invention also describes a prosthesis comprising an animal,  
XX metal or synthetic material, where the surface is coated with the  
XX polypeptide, a cosmetic material comprising the polypeptide, an elastic  
XX material comprising the polypeptide, a high tensile strength material  
XX comprising the polypeptide, a material comprising two or more  
XX polypeptides selected from (a) a polypeptide consisting essentially of a  
XX portion of the polypeptide comprising at least three beta sheet/beta turn  
XX structures, (b) a polypeptide consisting essentially of a portion of the  
XX amino acid sequence of an animal elastin comprising at least three beta  
XX sheets/beta turns, (c) a polypeptide consisting essentially of a portion  
XX of lamprin comprising at least three beta sheets/beta turns, and (d) a  
XX polypeptide consisting essentially of a spider silk protein comprising at  
XX least three beta sheets/beta turns, a polypeptide having the primary  
XX structure of a portion of a naturally occurring fibrous protein and a

CC secondary structure comprising at least three beta sheets/beta turns,  
CC where each of the beta sheet/beta turn structures comprises from 3 to  
CC about 7 amino acids and the polypeptide is not a naturally occurring  
CC fibrous protein. The minimal functional unit (MFU) of the invention is  
CC useful to construct human elastin-like prostheses such as tubes for blood  
CC vessel replacement and sheets for other uses such as wound or burn  
CC healing. Alternatively the MFU can be co-aggregated with other proteins,  
CC for example collagen, to provide prosthesis material that resembles the  
CC natural structural materials of the body. The MFU based material is  
CC subject to infiltration of cells growing in the patient, including  
CC endothelial cells, and the prosthesis can become a permanent living  
CC tissue replacement. The material is more biocompatible than other elastin  
CC -containing materials proposed for prostheses.  
XX  
XX Sequence 731 AA;

Query Match 97.2%; Score 908.5; DB 7; Length 731;  
Best Local Similarity 84.7%; Pred. No. 7.5e-56;  
Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
QY 1 AAGLIGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGA----- 41  
Db 516 AAGLIGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGA----- 575  
QY 42 -----VPGALAAKAAKYGAAPVGLGGLGALGVGIPGGVAGPAAAAA 87  
Db 576 SSSQHLPTSPSSPRVPGALAAKAAKYGAAPVGLGGLGALGVGIPGGVAGPAAAAA 635  
QY 88 AAKAAKAAQFGLVGAAGLGGVGLGVGVPGLGIPPAKAAKAAKYGAAGLGGVGG 147  
Db 636 AAKAAKAAQFGLVGAAGLGGVGLGVGVPGLGIPPAKAAKAAKYGAAGLGGVGG 695  
QY 148 AGQFPLGGVAARPGFGLSPFPFGACLGKACGRKK 183  
Db 696 AGQFPLGGVAARPGFGLSPFPFGACLGKACGRKK 731

RESULT 15  
AAR56653  
ID AAR56653 standard; protein; 733 AA.  
XX  
AC AAR56653;  
XX  
DT 25-MAR-2003 (revised)  
DT 22-MAR-1995 (first entry)  
XX  
DE Synthetic human tropoelastin (SHEL).  
XX Tropoelastin; pharmaceutical; surgical dressing.  
OS Synthetic.  
XX  
XX WO9414958-A1.  
XX  
PD 07-JUL-1994.  
XX  
PF 16-DEC-1993; 93WO-AU0000655.  
XX  
PR 22-DEC-1992; 92AU-00006520.  
PR 28-JUN-1993; 93AU-00009661.  
XX  
PA (UNSY ) UNIV SYDNEY.  
XX  
PI Weiss AS, Martin SL;  
XX  
DR WPI; 1994-263633/32.  
DR N-PSDB; AAQ70941.  
XX  
XX Synthetic polynucleotide(s) - encode recombinant tropoelastins and  
XX variants.  
XX  
PS Disclosure; Page 30; 77pp; English.  
XX

CC Human synthetic tropoelastin is susceptible to hydrolytic breakdown of  
CC the crosslinks. Such material may be useful in e.g. surgical  
CC applications, where the gradual loss of material over time is intended.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 733 AA;  
Query Match 97.2%; Score 908.5; DB 2; Length 733;  
Best Local Similarity 84.7%; Pred. No. 7.5e-56;  
Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFCA----- 41  
Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFCA----- 577  
QY 42 -----VPCALAAAKAAKYGAAPVGLGGLGALGVGIPGGVVGAGPAAAAA 87  
Db 578 SSSQHLPTSPSSPRVFGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVVGAGPAAAAA 637  
QY 88 AAKAAAKAAQFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPPAAAAAKAAKYGAAGLGVVGG 147  
Db 638 AAKAAAKAAQFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPPAAAAAKAAKYGAAGLGVVGG 697  
QY 148 AGQFPLGGVAARPGFGLSPIPPGACLGKACGRKK 183  
Db 698 AGQFPLGGVAARPGFGLSPIPPGACLGKACGRKK 733

RESULT 16  
AAV01301  
ID AAV01301 standard; protein; 733 AA.  
AC AAV01301;  
XX 07-JUN-1999 (first entry)  
XX Amino acid sequence of synthetic human tropoelastin SHEL.  
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL.  
XX Synthetic.  
OS Homo sapiens.  
XX WO9903886-A1.  
XX 28-JAN-1999.  
XX 17-JUL-1998; 98WO-AU000564.  
XX 18-JUL-1997; 97AU-00008117.  
XX (UNSY ) UNIV SYDNEY.  
XX Weiss AS;  
XX WPI; 1999-132162/11.  
XX N-PSDB; AAX27704.  
XX New derivatives of human tropoelastin - with elastin-like or  
PT macromolecular binding properties, useful e.g. as surgical implants.  
XX Disclosure; Fig 1; 82pp; English.  
XX The invention relates to a derivative or variant of human tropoelastin  
CC (hTE) having elastin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives  
CC or hybrid proteins containing the derivatives are useful in medical,  
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial

CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26A, from hTE. The present sequence represents the amino acid  
CC sequence of the synthetic human tropoelastin SHEL  
XX SQ Sequence 733 AA;

Query Match 97.2%; Score 908.5; DB 2; Length 733;  
Best Local Similarity 84.7%; Pred. No. 7.5e-56;  
Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFCA----- 41  
Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFCA----- 577  
QY 42 -----VPCALAAAKAAKYGAAPVGLGGLGALGVGIPGGVVGAGPAAAAA 87  
Db 578 SSSQHLPTSPSSPRVFGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVVGAGPAAAAA 637  
QY 88 AAKAAAKAAQFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPPAAAAAKAAKYGAAGLGVVGG 147  
Db 638 AAKAAAKAAQFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPPAAAAAKAAKYGAAGLGVVGG 697  
QY 148 AGQFPLGGVAARPGFGLSPIPPGACLGKACGRKK 183  
Db 698 AGQFPLGGVAARPGFGLSPIPPGACLGKACGRKK 733

RESULT 17  
ABG75223  
ID ABG75223 standard; protein; 757 AA.  
AC ABG75223;  
XX 12-FEB-2004 (first entry)  
XX Human tropoelastin protein.  
XX Human; tropoelastin; elastin; body vessel occlusion; stenosis;  
KW vascular smooth muscle cell; elastin signaling; vasotropic.  
XX Homo sapiens.  
XX WO2003082203-A2.  
XX 09-OCT-2003.  
XX 27-MAR-2003; 2003WO-US009391.  
XX 27-MAR-2002; 2002US-0368084P.  
XX (UTAH ) UNIV UTAH RES FOUND.  
XX Li DY, Karnik S;  
XX WPI; 2003-833516/77.  
XX Use of an agent that promotes elastin signaling in smooth muscle cells  
PT for e.g. decreasing or preventing occlusion of a body vessel by smooth  
PT muscle cells, treating or preventing obstructive vascular disease, or  
PT preventing stenosis.  
XX Claim 24; Page 138-141; Opp; English.  
XX The present invention relates to the use of an agent that promotes  
CC elastin signaling in smooth muscle cells for decreasing or preventing  
CC occlusion of a body vessel by smooth muscle cells, decreasing vascular  
CC obstruction, promoting actin stress fiber formation or actin  
CC polymerisation, increasing F:G actin ratio in a smooth muscle cell,  
CC treating or preventing obstructive vascular disease (e.g. restenosis), or  
CC preventing stenosis. The agent that promotes elastin signaling in smooth  
CC muscle cells is useful for decreasing or preventing occlusion of a body  
CC vessel by smooth muscle cells, decreasing vascular obstruction, promoting







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Db      573 GLGIPPAARAAKAY-----GVAARPGFGLSPIPPGACLGKACGR 614
Qy      181 KRK 183
      |||
Db      615 KRK 617
      |||

RESULT 21
AAB08630
ID AAB08630 standard; peptide; 712 AA.
XX AC AAB08630;
XX DT 20-DEC-2000 (first entry)
XX DE Amino acid sequence of a human elastin polypeptide.
XX DT
XX KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
XX KW smooth muscle cell differentiation; smooth muscle cell migration;
XX KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
XX KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
XX KW SVAS; hypertension; transplant arteriopathy.
XX OS Homo sapiens.
XX PN WO200050068-A2.
XX PD 31-AUG-2000.
XX PF 28-FEB-2000; 2000WO-US002526.
XX PR 26-FEB-1999; 99US-00258217.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Keating MT, Li DY;
XX DR WPI; 2000-533134/48.
XX PT Elastin based compositions useful for treating atherosclerosis,
XX PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
XX PT aneurysm, dissection SVAS and/or hypertension.
XX PS Example 3; Page 46; 79pp; English.
XX CC The present sequence represents a human elastin. Peptides derived from
XX CC elastin are used in compositions of the invention. The specification
XX CC describes elastin based compositions that are potent regulators of smooth
XX CC muscle cell proliferation, differentiation and migration in vivo. The
XX CC elastin-based compositions comprise at least one elastic fibre, elastins,
XX CC tropoelastins (or fragments of them) which have biological activities
XX CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;
XX CC stimulating the differentiation of smooth muscle cells in vivo; and
XX CC regulating the migration of smooth muscle cells in vivo. The compositions
XX CC by diminished capacity to regulate smooth muscle cell function such as
XX CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
XX CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
XX CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX CC
XX SQ Sequence 712 AA;

Query Match      87.9%; Score 822; DB 3; Length 712;
Best Local Similarity 90.2%; Pred. No. 8.3e-50;
Matches 165; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy      1 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPG 60
      |||
Db      548 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPG 607
      |||
Qy      61 VLGLGALGGVIGPGVVVGGAPAAAARAAKAAQAQFGLVGAAGLGLGVGGLGVPGVG 120
      |||
Db      608 VLGLGALGGVIGPGVVVGGAPAAAARAAKAAQAQFGLVGAAGLGLGVGGLGVPGVG 667
      |||

Qy      121 GLGIPPAARAAKAYGAAGLGGVGLGGAGQFPLGGVAARPGFGLSPIPPGACLGKACGR 180
      |||
Db      668 GLGIPPAARAAKAY-----GVAARPGFGLSPIPPGACLGKACGR 709
      |||
Qy      181 KRK 183
      |||
Db      710 KRK 712
      |||

RESULT 22
AAB08631
ID AAB08631 standard; peptide; 730 AA.
XX AC AAB08631;
XX DT 20-DEC-2000 (first entry)
XX DE Fusion protein comprising human elastin and c-myc.
XX DT
XX KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
XX KW smooth muscle cell differentiation; smooth muscle cell migration;
XX KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
XX KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
XX KW SVAS; hypertension; transplant arteriopathy.
XX OS Synthetic.
XX OS Homo sapiens.
XX OS Unidentified.
XX PN WO200050068-A2.
XX PD 31-AUG-2000.
XX PF 28-FEB-2000; 2000WO-US002526.
XX PR 26-FEB-1999; 99US-00258217.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Keating MT, Li DY;
XX DR WPI; 2000-533134/48.
XX PT Elastin based compositions useful for treating atherosclerosis,
XX PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
XX PT aneurysm, dissection SVAS and/or hypertension.
XX PS Example 3; Page 48; 79pp; English.
XX CC The present sequence represents a fusion protein, comprising human
XX CC elastin and c-myc, preceded by a His tag. The protein is used in
XX CC compositions of the invention. The specification describes elastin based
XX CC compositions that are potent regulators of smooth muscle cell
XX CC proliferation, differentiation and migration in vivo. The elastin-based
XX CC compositions comprise at least one elastic fibre, elastins, tropoelastins
XX CC (or fragments of them) which have biological activities comprising:
XX CC inhibiting the proliferation of smooth muscle cells in vivo; stimulating
XX CC the differentiation of smooth muscle cells in vivo; and regulating the
XX CC migration of smooth muscle cells in vivo. The compositions may be used
XX CC for the prophylaxis or treatment of a disorder characterized by
XX CC diminished capacity to regulate smooth muscle cell function such as
XX CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
XX CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
XX CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX CC
XX SQ Sequence 730 AA;

Query Match      87.9%; Score 822; DB 3; Length 730;
Best Local Similarity 90.2%; Pred. No. 8.5e-50;
Matches 165; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy      1 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPG 60

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XX 17-JUL-1998; 98WO-AU000564.
XX 18-JUL-1997; 97AU-00008117.
XX (UNSY ) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 1999-132162/11.
XX N-PSDB; AAX27707.
XX New derivatives of human tropoelastin - with elastin-like or
XX PT macromolecular binding properties, useful e.g. as surgical implants.
XX PS Claim 15; Fig 8; 82pp; English.
XX CC The invention relates to a derivative or variant of human tropoelastin
XX CC (hTE) having elastin-like and/or macromolecule (specifically
XX CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX CC comprising the nucleic acids encoding the variants or derivatives are
XX CC used to produce the proteins recombinantly. The tropoelastin derivatives
XX CC or hybrid proteins containing the derivatives are useful in medical,
XX CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX CC wrinkle or hand lotions, also as surgical implants, foods and industrial
XX CC products. The hybrid protein have controllable GAG-binding properties,
XX CC depending on presence or absence of a specific fragment, designated
XX CC peptide 26A, from hTE. The present sequence represents a human
XX CC tropoelastin derivative SHELgamma
XX SQ Sequence 200 AA;

Query Match      85.7%; Score 801; DB 2; Length 200;
Best Local Similarity 82.2%; Pred No. 8.3e-49;
Matches 162; Conservative 1; Mismatches 10; Indels 24; Gaps 1;

QY 11 GLGVGVPGVLGVGAGVPLGVGA-----GVPGGAVPGAL 46
Db 4 GALVGLGVPLGVGAGVPGFAGAGDEGVRRLSPELREGDPSSQHLPTSPSPVPGAL 63
QY 47 AAACAAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAAAATAAQAQFGLVGAAGL 106
Db 64 AAACAAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAAAATAAQAQFGLVGAAGL 123
QY 107 GGLGVGLGVPGVGGGLGIPPAATAAAYGAAAGLGGVILGGAGQPLGGVAARPFGGLSP 166
Db 124 GGLGVGLGVPGVGGGLGIPPAATAAAYGAAAGLGGVILGGAGQPLGGVAARPFGGLSP 183
QY 167 IFPGGACLGKACGRKRK 183
Db 184 IFPGGACLGKACGRKRK 200

RESULT 25
RAY01304
ID AAY01304 standard; protein; 147 AA.
XX AC AAY01304;
XX XX 07-JUN-1999 (first entry)
XX DE Human tropoelastin derivative SHELgamma.
XX KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
XX KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
XX KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO9903886-A1.
XX XX 28-JAN-1999.
PD

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XX 17-JUL-1998; 98WO-AU000564.
XX 18-JUL-1997; 97AU-00008117.
XX (UNSY ) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 1999-132162/11.
XX N-PSDB; AAX27706.
XX New derivatives of human tropoelastin - with elastin-like or
XX PT macromolecular binding properties, useful e.g. as surgical implants.
XX PS Claim 19; Fig 7; 82pp; English.
XX CC The invention relates to a derivative or variant of human tropoelastin
XX CC (hTE) having elastin-like and/or macromolecule (specifically
XX CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX CC comprising the nucleic acids encoding the variants or derivatives are
XX CC used to produce the proteins recombinantly. The tropoelastin derivatives
XX CC or hybrid proteins containing the derivatives are useful in medical,
XX CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX CC wrinkle or hand lotions, also as surgical implants, foods and industrial
XX CC products. The hybrid protein have controllable GAG-binding properties,
XX CC depending on presence or absence of a specific fragment, designated
XX CC peptide 26A, from hTE. The present sequence represents a human
XX CC tropoelastin derivative SHELgamma excluding the product encoded by exon
XX CC 26A
XX SQ Sequence 147 AA;

Query Match      78.0%; Score 729; DB 2; Length 147;
Best Local Similarity 99.3%; Pred No. 7.1e-44;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 40 GAVPGALAAAKAAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAAAATAAQAQFG 99
Db 4 GGVPGALAAAKAAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAAAATAAQAQFG 63
QY 100 LVGAAGLGGVLGGVPGVGGGLGIPPAATAAAYGAAAGLGGVILGGAGQPLGGVAAR 159
Db 64 LVGAAGLGGVLGGVPGVGGGLGIPPAATAAAYGAAAGLGGVILGGAGQPLGGVAAR 123
QY 160 PFGGLSPIFFPGGACLGKACGRKRK 183
Db 124 PFGGLSPIFFPGGACLGKACGRKRK 147

RESULT 26
RAY69137
ID AAY69137 standard; protein; 171 AA.
XX AC AAY69137;
XX XX 30-MAY-2000 (first entry)
XX DE Amino acid sequence of a human tropoelastin derivative.
XX KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
XX KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
XX KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
XX OS Homo sapiens.
XX OS WO200004043-A1.
XX PN 27-JAN-2000.
XX XX 19-JUL-1999; 99WO-AU000580.
XX XX 17-JUL-1998; 98AU-00004723.
PD

```

10-DEC-2001; 2001US-0339739P.  
PR 11-DEC-2001; 2001US-0339453P.  
PR 14-MAR-2002; 2002US-0365091P.  
PR 14-MAR-2002; 2002US-0365384P.  
PR 12-APR-2002; 2002US-0372381P.  
PR 12-APR-2002; 2002US-0372615P.  
PR 22-APR-2002; 2002US-00128558.  
PR 24-APR-2002; 2002US-0376045P.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
XX  
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
PI  
XX  
WPI; 2003-569235/53.  
DR N-PSDB; ADE07616.  
DR  
XX  
New polynucleotides, useful for expressing recombinant proteins for  
XX  
analysis, characterization or therapeutic use, or as markers for tissues  
PT  
PT in which the corresponding protein is preferentially expressed.  
XX  
XX  
Claim 20; SEQ ID NO 1593; 1177pp; English.  
PS  
XX  
The invention comprises the amino acid and coding sequences of novel  
CC  
proteins. The DNA and protein sequences of the invention are useful as:  
CC  
markers for tissues in which the corresponding protein is preferentially  
CC  
expressed; as molecular weight markers on gels; as chromosome markers or  
CC  
tags; to identify chromosomes or to map related gene positions; and to  
CC  
compare with endogenous DNA sequences in patients to identify potential  
CC  
genetic disorders. The present amino acid sequence represents a protein  
CC  
of the invention.  
XX  
XX  
Sequence 870 AA;  
SQ  
  
Query Match 73.3%; Score 685; DB 7; Length 870;  
Best Local Similarity 61.8%; Pred. No. 3.9e-40;  
Matches 154; Conservative 3; Mismatches 10; Indels 82; Gaps 5  
  
QY 1 AAAGLGAGIPGLGVGVGVPGVLGVGAGVPGVLGVGAGVPGFAGVPGALAAKAAKY----- 54  
Db 613 AAAGLGAGIPGLGVGVGVPGVLGVGAGVPGVLGVGAGVPGFAGVPGALAAKAAKYGLPLPPR 672  
QY 55 -----GAAVP 59  
Db 673 ASPEDVAVPQPLHLALWQPLARLTLSVAPEFLASCEQRWEVEDSPDPPTSRAGAAVP 732  
QY 60 GVLGGLGALGGVIGIPGVGVGAGPAAAAAATAKAAKAAQFG---LVGAAGLGGVLGVGG 115  
Db 733 GVLGGLGALGGVIGIPGVGVGAGPAAAAAATAKAAKAAQFGEHVVVGAAA----- 782  
QY 116 VEVGVLGGIIPAAAAKAAKYAAGLGGVLGGAGQFPLGGVAARPGFGLSPFPGG---A 172  
Db 783 --RPPGPGIPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPFPGSELFP 840  
QY 173 CLGKACGRK 181  
Db 841 C--ASCGR 847  
  
RESULT 28  
ADE56670  
ID ADE56670 standard; protein; 864 AA.  
XX  
AC ADE56670;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein Q99372, SEQ ID NO 2524.  
XX  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
XX



[illegible]

RESULT 30	
AB88422	
D	AAF88422 standard; protein; 472 AA.
X	
C	AAF88422;
X	
X	
T	23-MAY-2001 (first entry)
X	
X	Human membrane or secretory protein clone PSEC0191.
E	
X	Human; secretory protein; membrane protein; vaccine; gene therapy;
W	rheumatoid arthritis; diabetes.
X	
X	
S	Homo sapiens.
X	
N	EP1067182-A2.
N	
X	
D	10-JAN-2001.
D	
X	
F	07-JUL-2000; 2000EP-00114090.
X	
R	08-JUL-1999; 99JP-00194179.
R	11-JAN-2000; 2000JP-00118775.
R	02-MAY-2000; 2000JP-00183766.
R	
X	
X	
A	(HELI-) HELIX RES INST.
X	
X	Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
I	
I	WPI; 2001-0933989/11.
X	N-PSDB; AAF93849.
R	
R	
X	Nucleic acids encoding secretory proteins/membrane proteins, useful in
T	gene therapy or as candidate target molecules in drug development.
T	
PS	Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
X	
X	
X	This invention relates to nucleic acid sequences AAF93744 - AAF93916
X	which encode human secretory or membrane proteins represented by AAB88317
C	- AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
C	AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
C	invention. The invention also includes methods for the production of
C	antibodies directed against the proteins, and cDNA sequences, which can
C	be used in vaccines. The polynucleotide sequences can be used in gene
C	therapy. The polynucleotide sequences and the proteins they encode may be
C	used in vaccines.



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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:37:11 ; Search time 29.8873 Seconds  
(without alignments)  
2168.321 Million cell updates/sec

Title: US-09-743-818A-74

Perfect score: 935

Sequence: 1 AAAGLGAGIPGLGVGVGPG.....LSPFFGACLGKACGRKK 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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20: /cgn2\_6/ptodata/2/pubpaa/US10K\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	935	100.0	692	15	US-10-210-172-40
2	935	100.0	730	10	US-09-961-403-8
3	927	99.1	663	15	US-10-108-260A-2477
4	908.5	97.2	731	10	US-09-964-662-1
5	822	87.9	617	14	US-10-104-047-2915
6	819	87.6	711	15	US-10-210-172-38
7	307.5	32.9	696	8	US-08-806-029-36
8	307.5	32.9	696	15	US-10-441-965-23
9	307.5	32.9	750	8	US-08-806-029-25
10	304.5	32.6	696	15	US-10-441-965-21
11	304.5	32.6	1465	14	US-10-096-986-74
12	301.5	32.2	312	8	US-08-806-029-34
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Sequence 6, Appl  
Sequence 4, Appl  
Sequence 41, Appl



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Qy	98		AKAAKAAQA QFLVGAAGLGGLGVGGLVGPGVGGVGGIPPPAAA AKAAKYGAAGLCGVGG	147
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Qy	148		AGOPPLGVAARPGFGLSP IFFPGACICLKACGRKRK	183
Db	696		AGQPFLGVAARPFGLSPI FPFPGACILKACGRKRK	731
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US-10-104-047-2915				
; Sequence 2915, Application US/10104047				
; Publication No. US20030236392A1				
; GENERAL INFORMATION:				
; APPLICANT: HELIX RESEARCH INSTITUTE				
; TITLE OF INVENTION: NO. US20030236392alel full length cDNA				
; FILE REFERENCE: HI-A0105				
; CURRENT APPLICATION NUMBER: US/10/104,047				
; PRIOR FILING DATE: 2002-03-25				
; PRIOR APPLICATION NUMBER:				
; PRIOR FILING DATE:				
; NUMBER OF SEQ ID NOS: 4096				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 2915				
; LENGTH: 617				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
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Query Match 87.9%; Score 822; DB 14; Length 617;				
Best Local Similarity 90.2%; Pred.No. 1e-47;				
Matches 165; Conservative 0; Mismatches 0; Indels 18; Gaps 1;				
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Db	615		KRK 617	
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; Sequence 38, Application US/10210172				
; Publication No. US20040043928A1				
; GENERAL INFORMATION:				
; APPLICANT: Kekuda, Ramesh				
; APPLICANT: Miller, Charles				
; APPLICANT: Patturajan, Meera				
; APPLICANT: Pena, Carol				
; APPLICANT: Rieger, Daniel				
; APPLICANT: Shimkets, Richard				
; APPLICANT: Zerhusen, Bryan				
; APPLICANT: Li, Li				
; APPLICANT: Ji, Weizhen				
; APPLICANT: Padigaru, Muraliidhara				
; APPLICANT: Casman, Stacie				

## RESULT 8

## RESULT 8

APPLICANT: KUMAR, MANOJ

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 8.231 Seconds  
(without alignments)  
2139.188 Million cell updates/sec

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_79:\*  
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2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	908.5	97.2	792	1 EAHU	elastin precursor,
2	672	71.9	747	1 EABO	elastin precursor,
3	657	70.3	860	1 EAMS	elastin precursor,
4	655.5	70.1	770	2 S59623	tropoelastin - she
5	640	68.4	864	1 EART	elastin precursor
6	382.5	40.9	784	2 A26601	elastin precursor
7	265	28.3	641	1 QQBE31	nuclear antigen EB
8	243.5	26.0	718	2 A36068	major ampullate fi
9	232	24.8	767	2 F70895	hypothetical glyci
10	226	24.2	907	2 A45560	sporozoite surface
11	216	23.1	882	2 B70812	hypothetical glyci
12	214.5	22.9	212	2 E86179	hypothetical glyci
13	213.5	22.8	2639	2 T31328	hypothetical glyci
14	212	22.7	783	2 F70824	fibroin - Chinese
15	212	22.7	1901	2 F70806	hypothetical glyci
16	211	22.6	479	2 F70573	hypothetical glyci
17	211	22.6	741	2 G70917	hypothetical glyci
18	211	22.6	1329	2 F70917	hypothetical glyci
19	210.5	22.5	498	2 C70720	hypothetical glyci
20	209	22.4	749	2 A70812	hypothetical glyci
21	209	22.4	1489	2 D70807	hypothetical glyci
22	207.5	22.2	603	2 C70770	hypothetical glyci
23	207	22.1	268	2 B61615	hypothetical glyci
24	206	22.0	1381	2 F70806	hypothetical glyci
25	205.5	22.0	778	2 D70806	hypothetical glyci
26	205	21.9	525	2 F70878	hypothetical glyci
27	203.5	21.8	384	1 A26099	hypothetical glyci
28	203.5	21.8	618	2 A70989	hypothetical glyci
29	203.5	21.8	801	2 F70824	hypothetical glyci

30	203	21.7	496	2	H70839	hypothetical glyci
31	203	21.7	837	2	E70835	hypothetical glyci
32	202	21.6	1660	2	A70869	hypothetical glyci
33	200	21.4	162	2	S56703	glycine-rich cell
34	200	21.4	1306	2	A70934	hypothetical glyci
35	199	21.3	923	2	E70820	hypothetical glyci
36	197	21.1	447	2	G84687	probable disease r
37	196.5	21.0	408	2	S57483	glycine-rich protei
38	196	21.0	1538	2	H70846	hypothetical glyci
39	195.5	20.9	635	2	A57131	hypothetical glyci
40	195	20.9	1733	1	B45344	collagen alpha 2(V
41	195	20.9	1958	2	B40505	probable nuclear a
42	194.5	20.8	314	2	H70987	hypothetical prote
43	194.5	20.8	957	2	D70835	hypothetical glyci
44	193.5	20.7	396	2	T49109	hypothetical glyci
45	193.5	20.7	419	2	G70602	glycine-rich prote
46	193.5	20.7	667	2	A70893	hypothetical glyci
47	192.5	20.6	1079	2	B70807	hypothetical glyci
48	192	20.5	158	2	T08957	hypothetical glyci
49	192	20.5	615	2	H70589	glycine-rich prote
50	191.5	20.5	338	1	KNMU	hypothetical glyci
51	191.5	20.5	783	2	T35389	probable serine-th
52	191	20.4	439	2	D70954	hypothetical glyci
53	190.5	20.4	608	2	T05442	glycine-rich prote
54	190.5	20.4	743	1	S23779	collagen alpha 1(V
55	190	20.3	487	2	E70983	hypothetical glyci
56	190	20.3	694	2	F70868	hypothetical glyci
57	189.5	20.3	744	2	S15435	collagen alpha 1(V
58	189	20.2	576	2	A70900	hypothetical glyci
59	189	20.2	627	2	A44112	spidroin 2, dragli
60	188.5	20.2	562	2	B70953	hypothetical glyci
61	188.5	20.2	1758	2	T29350	hypothetical prote
62	188.5	20.2	1759	2	T29351	collagen alpha 2(I
63	187	20.0	255	2	B84777	hypothetical prote
64	187	20.0	584	2	G70804	hypothetical glyci
65	186.5	19.9	171	1	JBA041	chorion class B pr
66	185.5	19.8	744	1	A34246	collagen alpha 1(V
67	185.5	19.8	744	1	S23298	collagen alpha 1(V
68	185	19.8	245	2	F70787	hypothetical glyci
69	184.5	19.7	1373	1	A43291	collagen alpha 2(I
70	184	19.7	402	1	CGB02S	collagen alpha 2(I
71	184	19.7	491	2	D70916	hypothetical glyci
72	184	19.7	594	2	G70545	hypothetical glyci
73	184	19.7	606	2	H70816	hypothetical glyci
74	184	19.7	1763	2	S16366	collagen alpha 2(I
75	183.5	19.6	173	2	JQ1064	glycine-rich prote
76	183.5	19.6	256	2	A70514	hypothetical glyci
77	182.5	19.5	1669	1	CGHU4B	collagen alpha 1(I
78	182	19.5	463	2	B70893	hypothetical glyci
79	182	19.5	591	2	B70523	hypothetical glyci
80	182	19.5	853	2	A70896	hypothetical glyci
81	181	19.4	201	2	T00799	hypothetical prote
82	181	19.4	220	2	T14441	glycine-rich prote
83	181	19.4	469	2	A24450	collagen alpha 2(V
84	180.5	19.3	361	2	G70682	hypothetical glyci
85	180.5	19.3	731	2	C70974	hypothetical glyci
86	180	19.3	298	2	E95286	hypothetical glyci
87	180	19.3	2038	2	A43742	hypothetical prote
88	178.5	19.1	1669	1	CGMS4B	female sterile hom
89	178	18.9	532	2	F70580	collagen alpha 1(I
90	177	18.9	291	1	S31415	hypothetical glyci
91	177	18.9	484	2	G70846	glycine-rich prote
92	176.5	18.9	401	1	OZZQAC	hypothetical glyci
93	176.5	18.9	588	2	F70971	circumsporozoite p
94	176	18.8	271	2	S34666	hypothetical glyci
95	174.5	18.7	210	2	JQ1060	glycine-rich prote
96	174.5	18.7	461	2	F70571	glycine-rich prote
97	174	18.6	674	2	S23297	hypothetical glyci
98	174	18.6	1466	1	CGHU7L	collagen alpha 1(X
99	173.5	18.6	1011	2	F70620	collagen alpha 1(I
100	173.5	18.6	1366	1	CGHU2S	hypothetical glyci
						collagen alpha 2(I

## ALIGNMENTS

## RESULT 1

AHU  
 elastin precursor, long splice form - human  
 ;Alternate names: tropoelastin  
 ;Species: Homo sapiens (man)  
 ;Date: 22-Jun-1990 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 ;Accession: A32707; A30524; A53891  
 ;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.  
 ;Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987  
 ;Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cl  
 ;Reference number: A32707; MUID:87289668; PMID:3039501  
 ;Accession: A32707  
 ;Molecule type: mRNA  
 ;Residues: 1-500,507-792 <IND>  
 ;Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948  
 ;Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.  
 ;J. Biol. Chem. 264, 8887-8891, 1989  
 ;Title: Characterization of the complete human elastin gene. Delineation of unusual fea  
 ;Reference number: A33705; MUID:89255358; PMID:2722804  
 ;Accession: A33705  
 ;Molecule type: DNA  
 ;Residues: 1-27 <BAS>  
 ;Cross-references: GB:J04821; NID:g182052; PIDN:AA52379.1; PID:g553276  
 ;Fazio, M.J.; Olsen, D.R.; Kaub, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.  
 ;Invest. Dermatol. 91, 458-464, 1988  
 ;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant c  
 ;Reference number: A30524; MUID:89009960; PMID:3171221  
 ;Accession: A30524  
 ;Molecule type: mRNA  
 ;Residues: 1-453,483-617,651-792 <FAZ>  
 ;Cross-references: EMBL:M36660; NID:g182061; PIDN:AAA52382.1; PID:g182062  
 ;Note: this sequence represents a composite of several splice forms  
 ;Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.;  
 ;Lab. Invest. 58, 270-277, 1988  
 ;Title: Isolation and characterization of human elastin cDNAs, and age-associated varia  
 ;Reference number: A53891; MUID:88156138; PMID:2831431  
 ;Accession: A53891  
 ;Molecule type: mRNA  
 ;Residues: 164-453,483-500,507-617,651-792 <FAZ>  
 ;Cross-references: GB:M24782; NID:g182063; PIDN:AAA53190.1; PID:g182064  
 ;Comment: the term tropoelastin refers to a soluble precursor form of the extracellular  
 ;C:Genetics:  
 ;Gene: GDB:ELN  
 ;Cross-references: GDB:119107; OMIM:130160  
 ;Map position: 7q11.23-7q11.23  
 ;Superfamily: elastin  
 ;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine  
 ;F:1-26/Domain: signal sequence #status predicted <SIG>  
 ;F:27-792/Product: elastin #status predicted <MAT>  
 ;F:782-787/Disulfide bonds: #status predicted  
 ;Quality Match 97.2%; Score 908.5; DB 1; Length 792;  
 ;Best Local Similarity 84.7%; Pred. No. 5e-47;  
 ;Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
 ;  
 QY 1 AAGLGAIGPGLGVGVGVPGLVGVGAGVPGVLGVGVGVGFGA----- 41  
 Db 577 AARGLGAIGPGLGVGVGVPGLVGVGAGVPGVLGVGVGVGFGAGAGGVVRSLSPELRGDP 636  
 QY 42 -----VPCALAAAKAAYGAAVPGVLGGLGALGGVIGPGVGVGAGPAAAAA 87  
 Db 637 SSSQHLPSTSSPRVPFALAAAKAAYGAAVPGVLGGLGALGGVIGPGVGVGAGPAAAAA 696  
 QY 88 AAKAAAKAAQFGLVGAAGLGLGVGGGLVPGVGVGGIPPAKAAKAYGAAGLGVGG 147  
 Db 697 AAKAAAKAAQFGLVGAAGLGLGVGGGLVPGVGVGGIPPAKAAKAYGAAGLGVGG 756  
 QY 148 AGOFELGGVAARPGFGLSPIFFPGACLGKACGRK 183

757 AGOFPLGGVAARPGFGLSPIPPGGACLGKACGRKRK 792

## RESULT 2

EABO

elastin precursor, splice form a - bovine

N:Alternate names: tropoelastin

N:Contains: elastin precursor, splice form b; elastin precursor, splice form c

C:Species: Bos primigenius taurus (cattle)

C:Date: 08-Jun-1989 #sequence revision 26-Jul-1996 #text\_change 09-Jul-2004

C:Accession: A31865; A26728; B26728; A22343; I45886

E:Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams, Biochemistry 28, 2365-2370, 1989

A:Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing of the bovine elastin gene

A:Reference number: A31865; MUID:89274159; PMID:2543440

A:Accession: A31865

A:Molecule type: DNA

A:Residues: 1-27 <YEH>

A:Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:G340504; PIDN:AAA3077

R:Raju, K.; Anwar, R.A. J. Biol. Chem. 262, 5755-5762, 1987

A:Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of complementary DNAs

A:Reference number: A92640; MUID:87194772; PMID:3032943

A:Accession: A26728

A:Molecule type: mRNA

A:Residues: 1,'RS',4-11,'E',13-636,'V',638-747 <RAJ>

A:Cross-references: GB:J02717; NID:G163019; PIDN:AAA30503.1; PID:G163020

A:Accession: B26728

A:Molecule type: mRNA

A:Residues: 1,'RS',4-11,'E',13-225,240-636,'V',638-747 <RA2>

A:Cross-references: GB:K03505; NID:G163025; PIDN:AAA30505.1; PID:G163026

A:Accession: C26728

A:Molecule type: mRNA

A:Residues: 1,'RS',4-11,'E',13-225,260-636,'V',638-747 <RA3>

A:Cross-references: GB:K03506; NID:G163027; PIDN:AAA30506.1; PID:G163028

R:Ciccia, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbloom, J.C. Biochemistry 24, 3075-3080, 1985

A:Title: Structure of the 3' portion of the bovine elastin gene.

A:Reference number: A22343; MUID:85280426; PMID:2992576

A:Accession: A22343

A:Molecule type: DNA

A:Residues: 613-747 <CIC>

A:Cross-references: GB:M20415

R:Rosenbloom, J. Lab. Invest. 51, 605-623, 1984

A:Title: Biology of disease: Elastin: Relation of protein and gene structure to disease

A:Reference number: I45885; MUID:85059254; PMID:6150137

A:Accession: I45886

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 678-683,685-747 <ROS>

A:Cross-references: GB:M31898; NID:G163015; PIDN:AAA96417.1; PID:G163018

R:Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P. Biochem. Biophys. Res. Commun. 186, 549-555, 1992

A:Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an intramolecular disulfide bond

A:Reference number: A58621; MUID:92337651; PMID:1632791

A:Contents: annotation, disulfide bonds

C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix protein elastin

C:Genetics:

A:Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3

A:Note: the list of introns is incomplete

C:Superfamily: elastin

C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine

F:1-747/Product: elastin precursor, splice form a #status Predicted <EPA>

F:1-225,260-747/Product: elastin precursor, splice form c #status predicted <BPC>

F:1-225,240-747/Product: elastin precursor, splice form b #status predicted <BPB>

F:1-26/Domain: signal sequence #status predicted <SIG>

F:21-747/Product: elastin #status predicted <WAT>

F:105,109,152,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,651,652,702/disulfide bonds, #status experimental

Query Match 71.9%; Score 672; DB 1; Length 747;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 36.9996 Seconds  
(without alignments)  
2845.805 Million cell updates/sec

Title: US-09-743-818A-74  
Perfect score: 935  
Sequence: 1 AAGAGAGAGIGLVGVGVPG.....LSPIPPGACGLGACACRRK 183

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	935	100.0	258	2 QUMF5	Qumf5 homo sapien
2	935	100.0	730	1 ELS_HUMAN	P15502 homo sapien
3	930	99.5	643	2 Q8NB14	Q8NB14 homo sapien
4	908.5	97.2	757	2 Q14234	Q14234 homo sapien
5	908.5	97.2	757	2 Q75MU5	Q75MU5 homo sapien
6	908.5	97.2	757	2 AAS07435	AAS07435 homo sapi
7	822	87.9	570	2 Q6ZM06	Q6ZM06 homo sapien
8	822	87.9	570	2 BAC85506	BAC85506 homo sapi
9	822	87.9	687	2 Q14235	Q14235 homo sapien
10	818	87.5	687	2 Q7Z316	Q7Z316 homo sapien
11	815	87.2	711	2 Q7Z3F5	Q7Z3F5 homo sapien
12	814	87.1	658	2 Q6P0U4	Q6P0U4 homo sapien
13	814	87.1	658	2 AAH65566	AAH65566 homo sapi
14	728.5	77.9	707	2 Q28098	Q28098 bos taurus
15	682	72.9	666	2 Q28096	Q28096 bos taurus
16	663	70.9	747	1 ELS_BOVIN	P04985 bos taurus
17	657	70.3	810	2 Q9ES29	Q9ES29 mus musculu
18	657	70.3	860	1 ELS_MOUSE	P54320 mus musculu
19	657	70.3	860	2 Q8C9L8	Q8C9L8 mus musculu
20	640	68.4	864	1 ELS_RAT	Q99372 rattus norv
21	633	67.7	650	2 Q28099	Q28099 bos taurus
22	622.5	66.6	679	2 Q28097	Q28097 bos taurus
23	382	40.9	750	1 ELS_CHICK	P07916 gallus gall
24	365	39.0	472	2 Q8N2G0	Q8N2G0 homo sapien
25	351.5	37.6	602	2 Q15337	Q15337 homo sapien
26	351.5	37.6	635	2 Q15336	Q15336 homo sapien
27	307.5	32.9	559	2 Q6ZUN2	Q6ZUN2 homo sapien
28	307.5	32.9	559	2 BAC86188	BAC86188 homo sapi
29	295	31.6	100	1 ELS_SHEEP	P11547 ovis aries
30	266.5	28.5	1468	5 Q9GUB5	Q9GUB5 galliera me
31	265	28.3	641	1 EBN1_EBV	P03211 epstein-bar

32	265	28.3	641	2 Q777E1	Q777E1 human herpe
33	265	28.3	641	2 CAD53427	CAD53427 human her
34	263	28.1	738	2 Q02402	Q02402 pinctada fu
35	258.5	27.6	988	2 Q17434	Q17434 nephila cla
36	254.5	27.2	691	2 Q9BIU3	Q9BIU3 dolomeds t
37	249.5	26.7	644	2 Q8WSW4	Q8WSW4 nephila cla
38	248	26.5	447	2 Q9BIV1	Q9BIV1 argiope aur
39	247.5	26.5	544	2 Q46171	Q46171 nephila cla
40	243.5	26.0	651	2 Q9BIU9	Q9BIU9 argiope tri
41	243.5	26.0	747	1 SPD1_NEPCL	P19837 nephila cla
42	242	25.9	648	2 Q9BIU7	Q9BIU7 argiope tri
43	241.5	25.8	617	2 Q46172	Q46172 nephila cla
44	240	25.7	1002	2 Q9BIU8	Q9BIU8 argiope tri
45	239.5	25.6	524	2 Q817U1	Q817U1 araneus ven
46	237.5	25.4	1092	2 Q964R2	Q964R2 theileria t
47	232	24.8	767	2 Q79FT0	Q79FT0 mycobacteri
48	232	24.8	767	2 CAE55354	CAE55354 mycobacte
49	232	24.8	774	2 Q7U0P7	Q7U0P7 mycobacteri
50	231	24.7	429	2 Q817T9	Q817T9 araneus ven
51	230	24.6	294	2 Q16986	Q16986 araneus dia
52	229.5	24.5	360	2 Q16985	Q16985 araneus dia
53	228.5	24.4	563	2 Q6J6N0	Q6J6N0 araneus ven
54	228.5	24.4	563	2 AAT36347	AAT36347 araneus v
55	228	24.4	2655	2 Q964F4	Q964F4 antheraea y
56	226	24.2	907	2 Q26675	Q26675 theileria a
57	226	24.2	1460	2 Q7TWC3	Q7TWC3 mycobacteri
58	225.5	24.1	5263	1 FBOH_BOMMO	P05790 bombyx mori
59	223.5	23.9	443	2 Q9GUB4	Q9GUB4 galliera me
60	223.5	23.9	760	2 Q6PY84	Q6PY84 kukulcania
61	223.5	23.9	760	2 AAT08433	AAT08433 kukulcani
62	222	23.7	897	2 Q5Q294	Q5Q294 agelenopsis
63	222	23.7	897	2 AAT08436	AAT08436 agelenops
64	221.5	23.7	301	2 Q01927	Q01927 phytophthor
65	221.5	23.7	343	2 Q01914	Q01914 phytophthor
66	219.5	23.5	422	2 Q6Z142	Q6Z142 oryza sativ
67	219.5	23.5	422	2 BAC84308	BAC84308 oryza sat
68	218	23.3	360	2 Q9BIU0	Q9BIU0 latrodectus
69	217.5	23.3	400	2 Q8GTU0	Q8GTU0 oryza sativ
70	217.5	23.3	922	2 Q8MW53	Q8MW53 mytilus gal
71	217	23.2	797	2 Q7U1D4	Q7U1D4 mycobacteri
72	216	23.1	831	2 Q7U159	Q7U159 mycobacteri
73	216	23.1	879	2 Q8VKD2	Q8VKD2 mycobacteri
74	216	23.1	882	2 Q79FV6	Q79FV6 mycobacteri
75	216	23.1	882	2 CAE55329	CAE55329 mycobacte
76	215	23.0	783	2 Q7D9C6	Q7D9C6 mycobacteri
77	214.5	22.9	212	2 Q23018	Q23018 arabidopsis
78	214.5	22.9	1408	2 Q7U022	Q7U022 mycobacteri
79	214	22.9	347	2 Q01916	Q01916 phytophthor
80	214	22.9	626	2 Q9NHW1	Q9NHW1 nephila ina
81	214	22.9	749	2 Q7D974	Q7D974 mycobacteri
82	213.5	22.8	2639	2 Q76786	Q76786 antheraea p
83	213	22.8	284	2 Q6EE23	Q6EE23 euprosthen
84	213	22.8	907	2 Q44359	Q44359 nephila cla
85	213	22.8	1715	2 Q8V1Z0	Q8V1Z0 mycobacteri
86	213	22.8	1729	2 Q9U617	Q9U617 drosophila
87	212.5	22.7	349	2 Q9BIV0	Q9BIV0 argiope aur
88	212.5	22.7	486	2 Q9AR23	Q9AR23 oryza sativ
89	212	22.7	783	2 Q79FW8	Q79FW8 mycobacteri
90	212	22.7	783	2 CAE55316	CAE55316 mycobacte
91	212	22.7	1901	1 PG54_MYCTU	PG54_MYCTU mycobacte
92	211.5	22.6	501	2 Q7TZH0	Q7TZH0 mycobacteri
93	211.5	22.6	827	2 Q7P288	Q7P288 anopheles g
94	211.5	22.6	2249	2 Q9NHW4	Q9NHW4 nephila cla
95	211	22.6	479	2 Q06292	Q06292 mycobacteri
96	211	22.6	479	2 Q7U280	Q7U280 mycobacteri
97	211	22.6	603	2 Q7U079	Q7U079 mycobacteri
98	211	22.6	738	2 Q8VKL5	Q8VKL5 mycobacteri
99	211	22.6	741	2 Q79FP1	Q79FP1 mycobacteri
100	211	22.6	741	2 CAE55391	CAE55391 mycobacte

ALIGNMENTS







OX	NCBI_TaxID=9606;	OS	Homo sapiens (Human)
RN	[1]	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RP	SEQUENCE FROM N.A.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX	MEDLINE=87289668; PubMed=3039501;	OX	NCBI_TaxID=9606;
RA	Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,	RN	[1]
RA	Rosenbloom J.C., Peltonen L., Rosenbloom J.,	RP	SEQUENCE FROM N.A.
RA	"Alternative splicing of human elastin mRNA indicated by sequence	RX	MEDLINE=22737999; PubMed=12853948;
RT	analysis of cloned genomic and complementary DNA."	RA	Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RL	Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).	RA	Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RN	[2]	RA	Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RP	SEQUENCE FROM N.A.	RA	Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RX	MEDLINE=87274906; PubMed=3038460;	RA	Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA	Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,	RA	Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA	Rosenbloom J., Ornstein-Goldstein N.,	RA	Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RT	"Structure of the 3' region of the human elastin gene: great abundance	RA	Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RT	of Alu repetitive sequences and few coding sequences.";	RA	Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RL	Connect. Tissue Res. 16:197-211(1987).	RA	Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strommatt C.,
DR	EMBL; M17282; AAC98395.1; JOINED.	RA	Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
DR	EMBL; M16983; AAC98395.1; JOINED.	RA	Wendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
DR	EMBL; M17265; AAC98395.1; JOINED.	RA	Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
DR	EMBL; M17267; AAC98395.1; JOINED.	RA	Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
DR	EMBL; M17268; AAC98395.1; JOINED.	RA	Clifton S.W., Chisoe S.L., Maria M.A., Raymond C., Haugen E.,
DR	EMBL; M17270; AAC98395.1; JOINED.	RA	Gilllett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubbs K.,
DR	EMBL; M17271; AAC98395.1; JOINED.	RA	Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
DR	EMBL; M17272; AAC98395.1; JOINED.	RA	Baertsch R.A., Brent M.R., Keibler E., Fliecek P., Bork P., Suyama M.,
DR	EMBL; M17273; AAC98395.1; JOINED.	RA	Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
DR	EMBL; M17274; AAC98395.1; JOINED.	RT	Waterston R.H., Wilson R.K.;
DR	EMBL; M17275; AAC98395.1; JOINED.	RT	"The DNA sequence of human chromosome 7.";
DR	EMBL; M17276; AAC98395.1; JOINED.	RL	Nature 424:157-164(2003).
DR	EMBL; M17277; AAC98395.1; JOINED.	RN	[2]
DR	EMBL; M17278; AAC98395.1; JOINED.	RP	SEQUENCE FROM N.A.
DR	EMBL; M17279; AAC98395.1; JOINED.	RA	Waterston R.;
DR	EMBL; M17280; AAC98395.1; JOINED.	RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; M17281; AAC98395.1; JOINED.	RN	[3]
DR	GO: 0005578; C:extracellular matrix; NAS.	RP	SEQUENCE FROM N.A.
DR	GO: 0030023; F:extracellular matrix constituent conferring. . .; NAS.	RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR	InterPro: IPR001451; Hexapep_transf.	DR	EMBL; AC005056; AAS07435.1; .
DR	PRINTS; PR01500; TROPOLASTIN.	DR	InterPro: IPR001451; Hexapep_transf.
DR	PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN_1.	DR	InterPro: IPR003979; tropoelastin.
SQ	SEQUENCE 757 AA; 66136 MW; 237FE5B8A985CA8 CRC64;	DR	PRINTS; PR01500; TROPOLASTIN.
		DR	PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN_1.
		KW	Hypothetical protein.
		SQ	SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
	Query Match 97.2%; Score 908.5; DB 2; Length 757;		
	Best Local Similarity 84.7%; Pred. No. 6.7e-40;		
	Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;		
QY	1 AAGLGAGIPGLGVGVGVPGLGVGAGVPGVGLGVGAGVPGFCA-----41	QY	1 AAGLGAGIPGLGVGVGVPGLGVGAGVPGVGLGVGAGVPGFCA-----41
Db	542 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVGLGVGAGVPGFAGADEGVRRSLSPELREGDP 601	Db	542 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVGLGVGAGVPGFAGADEGVRRSLSPELREGDP 601
QY	42 -----VPGALAAAKAAYGAAVPGVGLGALGVGIPGGVVGAGPAAAAA 87	QY	42 -----VPGALAAAKAAYGAAVPGVGLGALGVGIPGGVVGAGPAAAAA 87
Db	602 SSSQHLPTSSPRVPGALAAAKAAYGAAVPGVGLGALGVGIPGGVVGAGPAAAAA 661	Db	602 SSSQHLPTSSPRVPGALAAAKAAYGAAVPGVGLGALGVGIPGGVVGAGPAAAAA 661
QY	88 AAKAAKAAQFGLVGAAGLGGVGLGVGIPGGVGLGIPPAATAAKAAYGAAAGLGVVGG 147	QY	88 AAKAAKAAQFGLVGAAGLGGVGLGVGIPGGVGLGIPPAATAAKAAYGAAAGLGVVGG 147
Db	662 AAKAAKAAQFGLVGAAGLGGVGLGVGIPGGVGLGIPPAATAAKAAYGAAAGLGVVGG 721	Db	662 AAKAAKAAQFGLVGAAGLGGVGLGVGIPGGVGLGIPPAATAAKAAYGAAAGLGVVGG 721
QY	148 AGOPFLGGVAARPFGLSPIFFPGGACLGKACGRKK 183	QY	148 AGOPFLGGVAARPFGLSPIFFPGGACLGKACGRKK 183
Db	722 AGOPFLGGVAARPFGLSPIFFPGGACLGKACGRKK 757	Db	722 AGOPFLGGVAARPFGLSPIFFPGGACLGKACGRKK 757
	RESULT 5		
ID	Q75MUS		
AC	Q75MUS; PRELIMINARY; PRT; 757 AA.		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein ELN.		
GN	Name=ELN;		

02-MAR-2004 (TRENBLrel. 27, Last annotation update)  
DE Hypothetical protein ELN.  
GN  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22737999; PubMed=12853948;  
RA Hallier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,  
Wagner-McPherson C., Layman D., Maas J., Jaeger S.D., Walker R.,  
Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,  
Pewell G.A., DeLehaunty K.D., Miner T.B., Nash W.E., Cordes M., Du H.,  
Sun H., Edwards J., Bradshaw-Cordon H., Ali J., Andrews S., Isak A.,  
Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,  
Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,  
Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,  
Kozlovicz M.T., Eldred J., Williams D., Bedell J.A., Wardis E.R.,  
Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,  
Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,  
Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,  
Baerbach R.A., Brent M.R., Keilber E., Flieck P., Bork P., Suyama M.,  
Bailey J.A., Portnoy M.E., Torrens D., Chinwalla A.T., Gish W.R.,  
Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,  
Waterston R.H., Wilson R.K.;  
RT "The DNA sequence of human chromosome 7.";  
RL Nature 424:157-164(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RQ Du H., Rohlfing T., Strong C.;  
RT "The sequence of Homo sapiens BAC clone CTB-5LJ22.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RQ Waterston R.H.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RQ Waterston R.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RQ Wilson R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
RQ EMBL; AC005056; AAC07435.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 757 AA; 66106 MW; 2B24F95D8360738 CRC64;

Query Match 97.2%; Score 908.5; DB 2; Length 757;  
Best Local Similarity 84.7%; Pred. No. 6.7e-40;  
Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
  
QY 1 AAAGLGAGIPGLGVGVPGLGVGAGVPGVLGVGAGVPGFGA----- 41  
Db 542 AAAGLGAGIPGLGVGVPGLGVGAGVPGVLGVGAGVPGFGA----- 41

QY 42 -----VPGALAAAKAAKYCAAVPVGLGGVGLGAGVGIGVGVGAGPAAAAA 87  
Db 602 SSSQHLPSTSPSPRVPGALAAAKAAKYCAAVPVGLGGVGLGAGVPGFGA 661

QY 88 AKAAAKAAQFGLVGAAGLGLGVGSLGVGVPVGGVGGIGTTPAAAATAAKAYGAAGLVGG 147  
Db 662 AKAAAKAAQFGLVGAAGLGLGVGSLGVGVPVGGVGGIGTTPAAAATAAKAYGAAGLVGG 721

QY 148 AGQFFLGGVAARPGLSPIFFPGACLCGACGRKK 183  
Db 722 AGQFFLGGVAARPGLSPIFFPGACLCGACGRKK 757

RESULT 7  
Q6ZMJ6 PRELIMINARY; PRT; 570 AA.  
ID Q6ZMJ6  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DE Hypothetical protein FLJ16246.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RQ Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,  
Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,  
Irie R., Otsuki T., Saito H., Wakamatsu A., Ishii S., Yamamoto J.,  
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
Magatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,  
Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,  
Masuhito Y., Nagai K., Isozaki T.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK122731; BAC8506.1; -  
DR InterPro; IPR001451; Hexapeptidase.  
DR PRINTS; PR01500; TROPOLASTIN.  
DR PROSITE; PS00101; HEXAPEPTIDASES; UNKNOWN 1.  
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;

Query Match 87.9%; Score 822; DB 2; Length 570;  
Best Local Similarity 90.2%; Pred. No. 1.7e-35;  
Matches 165; Conservative 0; Mismatches 0; Indels 18; Gaps 1;  
  
QY 1 AAAGLGAGIPGLGVGVPGLGVGAGVPGVLGVGAGVPGFGA----- 60  
Db 406 AAAGLGAGIPGLGVGVPGLGVGAGVPGVLGVGAGVPGFGA----- 60

QY 61 VLGGLGALGGVGPVGGVGGVGAAPAAAAAQAQFLVGAAGLGLGVGSLGVGVPVGG 120  
Db 466 VLGGLGALGGVGPVGGVGGVGAAPAAAAAQAQFLVGAAGLGLGVGSLGVGVPVGG 525

QY 121 GLGGIPPPAAAAAQAQFLVGAAGLGGVGLGGAGQFPPLGVGAARPFGLSPIFFPGACLCGACGR 180  
Db 526 GLGGIPPPAAAAAQAQFLVGAAGLGGVGLGGAGQFPPLGVGAARPFGLSPIFFPGACLCGACGR 567

QY 181 KRK 183  
Db 568 KRK 570

RESULT 8  
BAC85506 PRELIMINARY; PRT; 570 AA.  
ID BAC85506  
DT 02-MAR-2004 (TRENBLrel. 27, Created)  
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
DE CDNA FLJ16246 f16, clone HCHON2001577, highly similar to Human elastin gene.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RQ Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,  
Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,  
Irie R., Otsuki T., Saito H., Wakamatsu A., Ishii S., Yamamoto J.,  
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

**QY**      1    AAAAGLGGATPGTGVCGVGPGLGVGAGVPGLGVGAGVPGFVGAVPGLALAAAKAAYKGAAPVG    60  
         |||||  
**Db**     523   AAAGLGGATPGTGVCGVGPGLGVGAGVPGLGVGAGVPGFVGAVPGLALAAAKAAYKGAAPVG    582  
         |||||  
**QY**     61    VLGGTGALGGVGTGGVVGAGPAAAAAATAQAQFLVGAAGLGGTGVGSLGWPGVG    120  
         |||||  
**Db**     583   VLGGTGALGGVGTGGVVGAGPAAAAAATAQAQFLVGAAGLGGTGVGSLGWPGVG    642  
         |||||  
**QY**     121   GLGGTPPAAAANKAAYKGAAGLVGGAGQPPLGGVVAARPFGSLSPITPPGACLGKACGR    180  
         |||||  
**Db**     643   GLGGTPPAAAANKAY-----GVAARPGFGLSPIFFGGACLGKACGR    684  
         |||||  
**QY**       181   KRK    183

RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Eye;
RA	Strausberg R.;
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC065566; AAH65566.1; -
DR	InterPro; IPR001451; Hexapep transf.
DR	InterPro; IPR003979; tropoelastin.
DR	PRINTS; PR01500; TROPOELASTIN.
DR	PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ	SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;
Query Match	
Best Local Similarity 87.1%; Score 814; DB 2; Length 658;	
Matches 164; Conservative 0; Mismatches 1; Indels 18; Gaps	
QY	1 AAGLGAGTIGLVGVGVPGVLGVGAGVPGVLGVGAGVPGFAGVPGALAAAKAAYGAAPG
Db	
QY	494 AAGLGAGTIGLVGVGVPGVLGVGAGVPGVLGVGAGVPGFAGVPGALAAAKAAYGAAPG
Db	
QY	61 VLGGLGAGLVGGVIGPGVVGAGPAAAAAAAATAAQAQFLVGAAGLGGVLGVGVLGVPGV
Db	
QY	554 VLGGLGAGLVGGVIGPGVVGAGPAAAAAAAATAAQAQFLVGAAGLGGVLGVGVLGVPGV
Db	
QY	121 GLGGIPPPAAAAAKAAYGAAGLVGGVLGGAGGQFLGGVAAAPFGGLSPIFFGGACLGKACGR
Db	
QY	614 GLGGIPPPAAAAAKAAY-----GVAAPGFGLSPIFFGGACLGKACGR
QY	181 KRK 183
Db	
QY	656 KRK 658
RESULT 13	
AAH65566	PRELIMINARY; PRT; 658 AA.
ID	AAH65566
AC	AAH65566;
DT	02-MAR-2004 (TrEMBLrel. 27, Created)
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE	ELN protein.
GN	ELN.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Eye;
RL	MEDLINE=32389257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,







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Query Match          70.9%; Score 663; DB 1; Length 747;
Best Local Similarity 72.3%; Pred.No. 3.6e-27;
Matches 141; Conservative 8; Mismatches 30; Indels 16; Gaps 4;

1  AAAGLCAGIGPGLGVGVGPGLGVGAGVPGGLGVGAGVPGFGAVPGALAAKAAKYGAAPVG 60
DB 557  AAAGLIPAGVPGGLGVGAGVPGGLGVGAGVPGGLGVGAGVPGFGAVPGTTLAAKAAKFGPGGVG 616

61  VLGGGLGALGGVPIPGGVGAGVPGAPAAAAKAAKAAQOFLGVGAAGLGGGLGVGGLG-VPGV 119
DB 617  ALGGVGLDGGAGIPGGVAGVVP-AAAAKAAKAAKAAQFGL---GGVGGGLGVGGLGAVPGA 672

120  GGGGGTTPPAAKAAKYGAAGLGGVGLGGAGQFPPLGGVAARPFGFLSPI-----F 168
DB 673  VGLGGVSPAAAAKAAKAFGAAGLGGVGLGAGQFPFVGGAGGLGVGGKPKFPGGALGALGF 732

169  PGGACILGKACGRKRK 183
DB 733  PGGACILGKSCGRKRK 747

RESULT 17
Q9ESZ9 PRELIMINARY; PRT; 810 AA.
ID Q9ESZ9
AC Q9ESZ9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ELN (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid:10090;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=129/sv;
RC Green E.D.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF289665; AAF99336.1; -
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR DR InterPro; IPR003979; tropoelastin.
DR DR PRINTS; PR01500; TROP0ELASTIN.
DR NON TER 1
FO SEQUENCE 810 AA: 62704 MW: 18D61ED5AD4F40A2 CRC64;

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	Query Match	70.3%;	Score 657;	DB 2;	Length 810;	
	Best Local Similarity	57.1%;	Pred. No. 7.8e-27;			
	Matches 145; Conservative	9;	Mismatches 28;	Indels	72;	Gaps 6
Qy	1	AAAGLGGAGIPGLGVGVPGLGVGAGVPGFGLGVGAGVPGF-----GAVPGALAAA	49			
Dd	558	AAAGLGAGVDFGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGAVP	617			
Qy	50	KAAKYGAA-----VPGVLGSLGALGGVGIPDGVVVGAG - PAAAAAATAKAAAKAQF	98			
Dd	618	KAAKYGAAGGLGPGGLGGPGGLGGPGGLGGAGVDFRVAGAPPPAAAAATATAKAAKAQY	677			
Qy	99	GLVGAAGL-----GGLGVGGLGVPCVGGVLGGIPPPAAAAAKAAY	136			
Dd	678	GLGAGAGLGGAGLGGAGLGGAGGTLGAGGLGAGGLGAGGLGAGGGVSPAAAAAKAAY	737			
Qy	137	GAAGLGGVLGGAGGAPPGLGGVAARPQFGLSPIPF-----	169			
Dd	738	GAAGLGGVL-GARPPGGVVAARPQFGLSPIYPGGGAGGLGVGKKPKPYGGALGALGY	796			
Qy	170	GCACLGKACGRKK	183			
Dd	797	GGGCFGKSCGRKK	810			

RESULT 18



[illegible]

DR	EMBL; M50647; AAA42269.1; --
DR	EMBL; J04035; AAA42268.1; --
DR	EMBL; M86372; AAA42271.1; --
DR	EMBL; M86365; AAA42271.1; JOINED.
DR	EMBL; M86363; AAA42271.1; JOINED.
DR	EMBL; M86364; AAA42271.1; JOINED.
DR	EMBL; M86366; AAA42271.1; JOINED.
DR	EMBL; M86371; AAA42271.1; JOINED.
DR	EMBL; M86376; AAA42272.1; --
DR	EMBL; M86373; AAA42272.1; JOINED.
DR	EMBL; M86375; AAA42272.1; JOINED.
DR	PIR; A36106; EART.
DR	RGD; 67394; Eln.
DR	InterPro; IPR003979; tropoelastin.
DR	PRINTS; PR01500; TROPOELASTIN.
KW	Alternative splicing; Connective tissue; Repeat; Signal;
KW	Structural protein.
FT	NON TER 1 1
FT	SIGNAL <1 21
FT	CHAIN 22 864
FT	DISULPID 854 859
FT	VARSPLIC 263 307
FT	By similarity.
FT	Missing (In isoform 2, isoform 5, isoform
FT	7 and isoform 8).
FT	/FTId=VSP_004244.
FT	Missing (In isoform 3, isoform 5, isoform
FT	6 and isoform 8).
FT	/FTId=VSP_004245.
FT	Missing (In isoform 4, isoform 6, isoform
FT	7 and isoform 8).
FT	/FTId=VSP_004246.
FT	SEQUENCE 864 AA; 72786 MW; 456894BB09E79FD4 CRC64;
QY	Query Match 68.4%; Score 640; DB 1; Length 864;
DB	Best Local Similarity 59.1%; Pred. No. 6.2e-26;
DB	Matches 146; Conservative 9; Mismatches 24; Indels 68; Gaps 9
QY	1 AAAGLGGAGLPGLVGVGVPGLGVGAGVPGVLGVGAGVPGF--GAVPGALAAAKAAYGAAG- 57
DB	622 AAAGLGGAGVPLGVGAGVPGVPGFAGAG--GFAGAGVPGFGAGVPGSLAASKAAYGAAG 679
QY	58 ---VPGVLGGALGGV-----GIPGVVGAGPAAAAAATAKAAQAQFLGVGA 104
DB	680 GLGGPGLGGPGLGGPGGPGGLGVPGGVAGGAF-AATAAATAKAAQAQYLGGAG 738
QY	105 GL-----GGLVGGILG---VPCVGGGLGPIPPAAAATAKAAKYGAAGLGG 143
DB	739 GLGAGGLGAGLGGAGLGGAGLGGAGGVIPGAVGLGVSPAAAATAKAAKYGAAGLGG 798
QY	144 VLGGAGQFPLGVVAARPFGLSPIFP-----GGACILGK 176
DB	799 VLGARPPGGVVAARPFGLSPIYPGGAGGLGVGGKKPKPYGGALGALGYQGCGCFGK 857
QY	177 ACGRKRK 183
DB	858 SCGRKRK 864
RESULT 21	
Q28099	PRELIMINARY; PRT; 650 AA.
ID Q28099	
AC Q28099:	
DT 01-NOV-1996 (TRENBLrel. 01, Created)	
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)	
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)	
OS Elastin-CBELL; NCBI gi: 163003 (Fragment).	
OC Bos taurus (Bovine).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC Bovinae; Bos.	
OX NCBI_TaxID=9913;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=65280426; PubMed=2992576;	

Biochemistry 24:3075-3080(1985).  
[2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=88028442; PubMed=3665402;  
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,  
RA Rosenbloom J.C., Cicilia G., Yoon K., Rosenbloom J.;  
RT "Sequence variation of bovine elastin mRNA due to alternative  
RT splicing";  
RL Coll. Relat. Res. 7:235-247(1987).  
DR EMBL; M19372; AAA30500.1; -  
DR EMBL; M1422; AAA30500.1; JOINED.  
DR EMBL; M19366; AAA30500.1; JOINED.  
DR EMBL; M19367; AAA30500.1; JOINED.  
DR EMBL; M19368; AAA30500.1; JOINED.  
DR EMBL; M19369; AAA30500.1; JOINED.  
DR EMBL; M19370; AAA30500.1; JOINED.  
DR EMBL; M19371; AAA30500.1; JOINED.  
DR EMBL; M22771; AAA30500.1; JOINED.  
DR EMBL; M22772; AAA30500.1; JOINED.  
DR EMBL; M22773; AAA30500.1; JOINED.  
DR EMBL; M22774; AAA30500.1; JOINED.  
DR EMBL; M22988; AAA30500.1; JOINED.  
GO; GO:0005578; C:extracellular matrix; IEA.  
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.  
DR InterPro; IPR003979; tropoelastin.  
FT PRINTS; PRO1500; TROPELASTIN.  
FT NON TER 1  
SQ SEQUENCE 679 AA; 57652 MW; EB3C019E3BD7618D CRC64;

Query Match 66.6%; Score 622.5; DB 2; Length 679;  
Best Local Similarity 68.2%; Pred. No. 4.3e-25;  
Matches 133; Conservative 8; Mismatches 25; Indels 29; Gap

QY 1 AAGLCGAGTGGTGVGVGPGVLGVGAGVCGPFGAVPGALAAAKAYGA  
DB 502 AAAGLPAGVPLGVGVGVGLGVGVGAGVGP-AAAAAKAAKAAQFGL-  
QY 61 VLGLGLGALGVGIPGGVWGAGPAAAAAKAAKAAQFGLVGAAGLGLGVGGLG-V  
DB 549 ALGGVGDLSGAGIPGGVAGVP-AAAAAKAAKAAQFGL---GVGSLGVGGI  
QY 120 GGLGGIPPPAAAAAKAYGAAGLGVLGGAGOFFPLGGVAARPFGLSPI-  
DB 605 VGLGGVSPAAAANKAFGAAGLVGLGAGQFPPIGGGAGGLGVGKPKPGGALGA  
QY 169 PGACILGKACGRKRK 183  
DB 665 PGACILGKSCGRKRK 679

RESULT 23  
ELB\_CHICK STANDARD; PRT; 750 AA.  
ID AC P07916;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Elastin precursor (tropoelastin) (Fragment).  
GN Name=EUN;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=87242320; PubMed=3593675;  
RA Bressan G.M., Argos P., Stanley K.K.;  
RT "Repeating structure of chick tropoelastin revealed by complementary  
RT DNA cloning.";  
RL Biochemistry 26:1497-1503(1987).  
RN [2]  
RN SEQUENCE OF 85-750 FROM N.A. (TSOFORM 2)



[illegible]

Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases. EMBL; AK125111; BAC86188.1; -

DR Inter-Pro; IP0031979; tropoelastin.

DR PRINTS; PR01500; TROPOLASTIN.

DR SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 32.9%; Score 307.5; DB 2; Length 559;

Best Local Similarity 39.6%; Pred. No. 8.3e-09;

Matches 107; Conservative 14; Mismatches 48; Indels 101; Gaps 17;

QY 2 AAGLG---AGTGLGV-----GVGVP-----GLGVGAGVPG 29

DB 174 APGVGAGAFIPGVPGFGPGQVPLPIKAPKLFGLPYTTGKLPYGVGPG-GVAG 232

QY 30 LGVGAGVP---GFGAVPFCALAAAK-AAKYGAAPVGVGLGALGGVGP-----GGVVG 79

DB 233 AAGKAGYPTGTGVGPQAAAAAARAKAFGAGAGVLPVGGAGVPGVPGAIPGIGGIAG 292

QY 80 AGPAAAAAARAKAAQFGLVGAAGL-----GGLGVGLGVPGVG---GLG-----123

DB 293 VGTFAAAAAAARAKAAKYG---AAAGLVPGPGFGPGVGVGAGVPGVPGAGIPVVP 350

QY 124 --GIPPA-----AAKAAYKA---AGLGGV--LG-GAGQFP-----LG 154

DB 351 GAGIPGAAPVGVSPAAAAAARAKAAYGARPGVGVGIGTYGVGAGGFPFGVGVGGIP 410

QY 155 GVAARPGFGLS-----PIFPGGAC 173

DB 411 GVAGVPGVGGSRRCPSGSHFPRSSGSSC 440

RESULT 28

BAC86188 PRELIMINARY; PRT; 559 AA.

ID BAC86188

AC BAC86188;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE CDNA FLJ43523 fis, clone PLACE5000282, weakly similar to Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

RT "NEO human cDNA sequencing project."

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK125111; BAC86188.1; -

DR SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 32.9%; Score 307.5; DB 2; Length 559;

Best Local Similarity 39.6%; Pred. No. 8.3e-09;

Matches 107; Conservative 14; Mismatches 48; Indels 101; Gaps 17;

QY 2 AAGLG---AGTGLGV-----GVGVP-----GLGVGAGVPG 29

DB 174 APGVGAGAFIPGVPGFGPGQVPLPIKAPKLFGLPYTTGKLPYGVGPG-GVAG 232

QY 30 LGVGAGVP---GFGAVPFCALAAAK-AAKYGAAPVGVGLGALGGVGP-----GGVVG 79

DB 233 AAGKAGYPTGTGVGPQAAAAAARAKAFGAGAGVLPVGGAGVPGVPGAIPGIGGIAG 292

QY 80 AGPAAAAAARAKAAQFGLVGAAGL-----GGLGVGLGVPGVG---GLG-----123

DB 293 VGTFAAAAAAARAKAAKYG---AAAGLVPGPGFGPGVGVGAGVPGVPGAGIPVVP 350

QY 124 --GIPPA-----AAKAAYKA---AGLGGV--LG-GAGQFP-----LG 154

DB 351 GAGIPGAAPVGVSPAAAAAARAKAAYGARPGVGVGIGTYGVGAGGFPFGVGVGGIP 410

QY 155 GVAARPGFGLS-----PIFPGGAC 173

DB 411 GVAGVPGVGGSRRCPSGSHFPRSSGSSC 440

RESULT 28

BAC86188 PRELIMINARY; PRT; 559 AA.

ID BAC86188

AC BAC86188;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE CDNA FLJ43523 fis, clone PLACE5000282, weakly similar to Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

RT "NEO human cDNA sequencing project."

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK125111; BAC86188.1; -

DR SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 32.9%; Score 307.5; DB 2; Length 559;

Best Local Similarity 39.6%; Pred. No. 8.3e-09;

Matches 107; Conservative 14; Mismatches 48; Indels 101; Gaps 17;

QY 2 AAGLG---AGTGLGV-----GVGVP-----GLGVGAGVPG 29

DB 174 APGVGAGAFIPGVPGFGPGQVPLPIKAPKLFGLPYTTGKLPYGVGPG-GVAG 232

QY 30 LGVGAGVP---GFGAVPFCALAAAK-AAKYGAAPVGVGLGALGGVGP-----GGVVG 79

DB 233 AAGKAGYPTGTGVGPQAAAAAARAKAFGAGAGVLPVGGAGVPGVPGAIPGIGGIAG 292

QY 80 AGPAAAAAARAKAAQFGLVGAAGL-----GGLGVGLGVPGVG---GLG-----123

DB 293 VGTFAAAAAAARAKAAKYG---AAAGLVPGPGFGPGVGVGAGVPGVPGAGIPVVP 350

QY 124 --GIPPA-----AAKAAYKA---AGLGGV--LG-GAGQFP-----LG 154

DB 351 GAGIPGAAPVGVSPAAAAAARAKAAYGARPGVGVGIGTYGVGAGGFPFGVGVGGIP 410

QY 155 GVAARPGFGLS-----PIFPGGAC 173

DB 411 GVAGVPGVGGSRRCPSGSHFPRSSGSSC 440

RESULT 28

BAC86188 PRELIMINARY; PRT; 559 AA.

ID BAC86188

AC BAC86188;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE CDNA FLJ43523 fis, clone PLACE5000282, weakly similar to Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

RT "NEO human cDNA sequencing project."

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK125111; BAC86188.1; -

DR SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 32.9%; Score 307.5; DB 2; Length 559;

Best Local Similarity 39.6%; Pred. No. 8.3e-09;

Matches 107; Conservative 14; Mismatches 48; Indels 101; Gaps 17;

QY 2 AAGLG---AGTGLGV-----GVGVP-----GLGVGAGVPG 29

DB 174 APGVGAGAFIPGVPGFGPGQVPLPIKAPKLFGLPYTTGKLPYGVGPG-GVAG 232

QY 30 LGVGAGVP---GFGAVPFCALAAAK-AAKYGAAPVGVGLGALGGVGP-----GGVVG 79

DB 233 AAGKAGYPTGTGVGPQAAAAAARAKAFGAGAGVLPVGGAGVPGVPGAIPGIGGIAG 292

QY 80 AGPAAAAAARAKAAQFGLVGAAGL-----GGLGVGLGVPGVG---GLG-----123

DB 293 VGTFAAAAAAARAKAAKYG---AAAGLVPGPGFGPGVGVGAGVPGVPGAGIPVVP 350

Db 61 GCAGGLGVGKPKPPFGGALGALGPPGGACLGKCKGRK 100  
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## RESULT 30

Q9GUB5 PRELIMINARY; PRT; 1468 AA.  
AC Q9GUB5;  
DT 01-MAR-2001 (TREMELrel. 16, Created)  
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)  
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)  
DE Heavy-chain fibroin (Fragment).  
GN Name=Fib-H;  
OS Galleria mellonella (Wax moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;  
OC Pyralidae; Galleriinae; Galleria.  
OX NCBI\_taxid=7137;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Posterior silk gland;  
RX MEDLINE=22063245; PubMed=11886872;  
RA Zurovec M., Sehnal F.;  
RT "Unique molecular architecture of silk fibroin in the waxmoth,  
RT Galleria mellonella.";  
RL J. Biol. Chem. 277:22639-22647(2002).  
DR EMBL; AF095239; AAG10393.1; -.  
FT NON TER 1468 1468  
SQ SEQUENCE 1468 AA; 122704 MW; 2DA59E1181BB3DDF CRC64;

Query Match 28.5%; Score 266.5; DB 2; Length 1468;  
Best Local Similarity 35.6%; Pred. No. 2e-06;  
Matches 83; Conservative 23; Mismatches 58; Indels 69; Gaps 10;  
QY 1 AAAGLGAGIPGLGVG-----VGVPGLG-----VGAGVPLGVG 33  
Db 280 AAGSAGAGLGGVGGSGSSAAGSAGSAGEVILIDRSSAASRAAAGSAGSGVG-G 338  
QY 34 AGVPFGAVP--GALAAAKAAYGAAVPGV---LGLGLGGLGVGIPG-----GVVG 79  
Db 339 LGLGLGPIGGIGPIGATSTSGAGLGGVGAAGSAGLGGGGAGSAGSAGAGLGGIG 398  
QY 80 AGPAAAAAATAAKAAQFGLV-----GAAAGLGLGVGGLVPGVGGGL 122  
Db 399 AGSGSGSSAASAGSAGSAGEVIVIDRSSAASRAAAGSAGSAGLGLGLGPGYGGIGL 458  
QY 123 GGIPTPAAAKAAYGAAGLGGVLCGAGQFPLGGVAARPGFGLSPIFFGGACLG 175  
Db 459 NGVSSASAL-----GAGLGGV-GTAGASGLGGIG---GAGVSAVGPAGAGLG 501

Search completed: November 19, 2004, 16:36:54  
Job time : 38.9996 secs





GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 16:37:11 ; Search time 2.12314 Seconds  
(without alignments)  
2168.321 Million cell updates/sec

Title: US-09-743-818a-13

Perfect score: 59

Sequence: 1 ALAAKAAKYGAA 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PUB.pcp.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PUB.pcp.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB\_PUB.pcp.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB\_PUB.pcp.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pcp.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09A\_NEW\_PUB\_PUB.pcp.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pcp.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB\_PUB.pcp.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB\_PUB.pcp.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB\_PUB.pcp.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	617	US-10-104-047-2915	Sequence 2915, Ap
2	59	100.0	663	US-10-108-260A-2477	Sequence 2477, Ap
3	59	100.0	692	US-10-210-172-40	Sequence 40, Appl
4	59	100.0	730	US-09-961-403-8	Sequence 8, Appl
5	59	100.0	731	US-09-964-662-1	Sequence 1, Appl
6	56	94.9	711	US-10-210-172-38	Sequence 38, Appl
7	49	83.1	144	US-10-424-599-269890	Sequence 9, Appl
8	46	78.0	117	US-09-964-662-9	Sequence 10, Appl
9	46	78.0	118	US-09-964-662-11	Sequence 11, Appl
10	46	78.0	199	US-09-964-662-11	Sequence 2, Appl
11	46	78.0	200	US-09-964-662-2	Sequence 12700, Ap
12	41	69.5	277	US-10-437-963-122700	Sequence 9086, Ap
13	40	67.8	378	US-10-369-493-9086	

14	39	66.1	342	14	US-10-369-493-19927	Sequence 19927, A
15	39	66.1	485	14	US-10-369-493-16900	Sequence 16900, A
16	39	66.1	569	13	US-10-078-929-116	Sequence 116, App
17	38	64.4	129	15	US-10-424-599-209451	Sequence 209451, A
18	38	64.4	149	9	US-09-738-626-6936	Sequence 6936, Ap
19	38	64.4	159	17	US-10-425-115-340008	Sequence 340008, A
20	38	64.4	177	16	US-10-437-963-163840	Sequence 163840, A
21	38	64.4	233	13	US-10-056-744B-4	Sequence 4, Appl
22	38	64.4	251	13	US-10-068-134-4	Sequence 4, Appl
23	38	64.4	463	14	US-10-369-493-9096	Sequence 9096, Ap
24	38	64.4	463	14	US-10-369-493-8449	Sequence 8449, Ap
25	37	62.7	86	17	US-10-425-115-221398	Sequence 221398, A
26	37	62.7	152	17	US-10-425-115-353761	Sequence 353761, A
27	37	62.7	152	17	US-10-425-115-353768	Sequence 353768, A
28	37	62.7	158	17	US-10-739-930-8468	Sequence 8468, Ap
29	37	62.7	177	17	US-10-425-115-353760	Sequence 353760, A
30	37	62.7	184	17	US-10-425-115-353770	Sequence 353770, A
31	37	62.7	192	16	US-10-437-963-123914	Sequence 123914, A
32	37	62.7	213	17	US-10-739-930-8462	Sequence 8462, Ap
33	37	62.7	385	14	US-10-156-761-12560	Sequence 12560, A
34	37	62.7	388	14	US-10-368-075-650	Sequence 650, App
35	37	62.7	452	14	US-10-369-493-17360	Sequence 17360, A
36	37	62.7	531	14	US-10-156-761-14639	Sequence 14639, A
37	37	62.7	698	14	US-10-017-161-1970	Sequence 1970, Ap
38	37	62.7	698	14	US-10-292-798-1618	Sequence 1618, Ap
39	37	62.7	902	15	US-10-437-963-138437	Sequence 138437, A
40	37	62.7	1589	16	US-10-424-599-153020	Sequence 153020, A
41	37	62.7	55	15	US-10-425-115-211597	Sequence 211597, A
42	36	61.0	71	17	US-10-437-963-164333	Sequence 164333, A
43	36	61.0	109	16	US-10-425-115-193612	Sequence 193612, A
44	36	61.0	111	17	US-10-425-115-267771	Sequence 267771, A
45	36	61.0	142	17	US-10-115-123-397	Sequence 397, App
46	36	61.0	194	14	US-10-115-123-397	Sequence 397, App
47	36	61.0	194	14	US-10-437-963-160892	Sequence 160892, A
48	36	61.0	196	15	US-10-051-874-95	Sequence 95, Appl
49	36	61.0	204	16	US-10-027-806-58	Sequence 58, Appl
50	36	61.0	217	15	US-10-027-801-58	Sequence 58, Appl
51	36	61.0	222	13	US-10-029-120-58	Sequence 58, Appl
52	36	61.0	222	13	US-10-099-322-303	Sequence 303, App
53	36	61.0	222	13	US-10-044-564-303	Sequence 303, App
54	36	61.0	222	14	US-10-369-493-15794	Sequence 15794, A
55	36	61.0	222	14	US-10-369-493-15426	Sequence 15426, A
56	36	61.0	224	14	US-10-437-963-201970	Sequence 201970, A
57	36	61.0	224	14	US-10-369-493-15426	Sequence 15426, A
58	36	61.0	235	14	US-10-437-963-160892	Sequence 160892, A
59	36	61.0	238	14	US-10-437-963-160892	Sequence 160892, A
60	36	61.0	244	14	US-10-437-963-160892	Sequence 160892, A
61	36	61.0	251	16	US-10-437-963-160892	Sequence 160892, A
62	36	61.0	274	9	US-09-738-626-6076	Sequence 6076, Ap
63	36	61.0	293	14	US-10-369-493-8030	Sequence 8030, Ap
64	36	61.0	295	9	US-09-816-028A-32	Sequence 32, Appl
65	36	61.0	295	14	US-10-303-161-32	Sequence 32, Appl
66	36	61.0	295	14	US-10-303-118-32	Sequence 32, Appl
67	36	61.0	295	14	US-10-303-128-32	Sequence 32, Appl
68	36	61.0	295	14	US-10-303-134-32	Sequence 32, Appl
69	36	61.0	295	14	US-10-303-162-32	Sequence 32, Appl
70	36	61.0	295	17	US-10-820-536-32	Sequence 32, Appl
71	36	61.0	295	17	US-10-845-408-32	Sequence 32, Appl
72	36	61.0	295	17	US-10-845-412-32	Sequence 32, Appl
73	36	61.0	295	17	US-10-846-219-32	Sequence 32, Appl
74	36	61.0	309	16	US-10-437-963-196196	Sequence 196196, A
75	36	61.0	330	16	US-10-437-963-196197	Sequence 196197, A
76	36	61.0	330	16	US-10-437-963-196197	Sequence 196197, A
77	36	61.0	388	9	US-09-738-626-5090	Sequence 5090, Ap
78	36	61.0	436	17	US-10-425-115-356194	Sequence 356194, A
79	36	61.0	575	15	US-10-425-114-45940	Sequence 45940, A
80	36	61.0	623	16	US-10-437-963-109127	Sequence 109127, A
81	36	61.0	688	16	US-10-437-963-152448	Sequence 152448, A
82	36	61.0	698	16	US-10-437-963-168409	Sequence 168409, A
83	36	61.0	766	15	US-10-282-122A-66102	Sequence 66102, A
84	36	61.0	845	15	US-10-424-599-206032	Sequence 206032, A
85	36	61.0	880	16	US-10-437-963-126058	Sequence 126058, A
86	36	61.0	890	16	US-10-437-963-177048	Sequence 177048, A
87	36	61.0	1257	15	US-10-282-122A-74310	Sequence 74310, A

87	36	61.0	1347	16	US-10-437-963-196404	Sequence 196404,
88	36	61.0	1444	16	US-10-437-963-177050	Sequence 177050,
89	36	61.0	3352	14	US-10-156-761-7961	Sequence 7961, Ap
90	35	59.3	83	17	US-10-437-963-167410	Sequence 167410,
91	35	59.3	96	17	US-10-425-115-254505	Sequence 254505,
92	35	59.3	107	16	US-10-437-963-135427	Sequence 135427,
93	35	59.3	122	9	US-09-815-242-13247	Sequence 13247, A
94	35	59.3	122	9	US-09-815-242-13568	Sequence 13568, A
95	35	59.3	122	15	US-10-386-050A-6	Sequence 6, Appli
96	35	59.3	122	15	US-10-386-050A-20	Sequence 20, Appl
97	35	59.3	127	15	US-10-389-566-1441	Sequence 1441, Ap
98	35	59.3	127	15	US-10-389-566-1270	Sequence 1270, Ap
99	35	59.3	127	16	US-10-282-1282A-74026	Sequence 74026, A
100	35	59.3	127	16	US-10-474-776-680	Sequence 680, App

## ALIGNMENTS

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RESULT 1
US-10-104-047-2915
; Sequence 2915, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2915
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2915

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Query Match          100.0%; Score 59; DB 14; Length 617;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ALAAKAAKYGA 13  
db 497 ALAAKAAKYGA 509

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RESULT 2
US-10-108-260A-2477
; Sequence 2477, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2477
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2477

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Query Match	100.0%;	Score 59;	DB 15;	Length 663;
Best Local Similarity	100.0%;	Pred. No. 0.048;		
Matches 13.	Conservative	0;	Mismatches 0;	Indels

Qy 1 ALAAAKAAKYGAA 13  
|||  
Db 525 ALAAAKAAKYGAA 53

Query Match 100.0%; Score 59; DB 15; Length 692;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 13; Conservative 0; Mismatches 0; Indels

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RESULT 3
US-10-210-172-40
Sequence 40, Application US/10210172-40
Publication No. US20040043928A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shmukes, Richard
APPLICANT: Zethusen, Bryan
APPLICANT: Li, Li
APPLICANT: Ji, Weizhen
APPLICANT: Padigaru, Muralidhara
APPLICANT: Casman, Stacie
APPLICANT: Voss, Edward
APPLICANT: Boldog, Ferenc
APPLICANT: Gorman, Linda
APPLICANT: Leite, Mario
APPLICANT: Vernet, Corine
APPLICANT: Anderson, David
APPLICANT: Guo, Xiaojia
APPLICANT: Zhong, Mei
APPLICANT: Gerlach, Valerie
APPLICANT: Hjal, Tord
APPLICANT: Rastelli, Luca
APPLICANT: Spytek, Kimberly
APPLICANT: Edinger, Shlomit
APPLICANT: Ellerman, Karen
APPLICANT: Malvankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsbrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYMER
FILE REFERENCE: 21402-416 A
CURRENT APPLICATION NUMBER: US/10/210-172-40
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/303,565
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,909
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,818
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/310,202
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,919
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,505
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,212
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,919
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,212
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,818
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data r
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuroSeqdist version 0.1
SEQ ID NO 40
LENGTH: 692
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-40

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PRIOR FILING DATE: 2001-08-16

Query Match 100.0%; Score 59; DB 15; Length 692;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13  
| | | | | | | | | |  
Db 554 ALAAAKAAYGAA 566

## RESULT 4

US-09-961-403-8  
; Sequence 8, Application US/09961403  
; Publication No. US20030077589A1  
; GENERAL INFORMATION:  
; APPLICANT: HE-STUMPP, HOLGER  
; APPLICANT: HAENDLER, BERNARD  
; APPLICANT: KRAETZSCHMAR, JOERN  
; APPLICANT: KREFT, BERTHOLT  
; APPLICANT: WINTERHAGER, ELKE  
; APPLICANT: REGIDOR, PEDRO  
; APPLICANT: SCOTTI, SIMONE  
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS  
; FILE REFERENCE: SCH-1789  
; CURRENT APPLICATION NUMBER: US/09/961,403  
; CURRENT FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 730  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-961-403-8

Query Match 100.0%; Score 59; DB 10; Length 730;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13  
| | | | | | | | | |  
Db 592 ALAAAKAAYGAA 604

## RESULT 5

US-09-964-662-1  
; Sequence 1, Application US/09964662  
; Publication No. US20030166846A1  
; GENERAL INFORMATION:  
; APPLICANT: PROTEIN SPECIALTIES LTD.  
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP  
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND  
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS  
; FILE REFERENCE: 041082/0112  
; CURRENT APPLICATION NUMBER: US/09/964,662  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: 09/340,736  
; PRIOR FILING DATE: 1999-06-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-662-1

Query Match 100.0%; Score 59; DB 10; Length 731;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13  
| | | | | | | | | |  
Db 593 ALAAAKAAYGAA 605

## RESULT 6

US-10-210-172-38  
; Sequence 38, Application US/10210172

; Publication No. US20040043928A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Pena, Carol  
; APPLICANT: Rieger, Daniel  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Li, Li  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Casman, Stacie  
; APPLICANT: Voss, Edward  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gorman, Linda  
; APPLICANT: Leite, Mario  
; APPLICANT: Vernet, Corine  
; APPLICANT: Anderson, David  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zhong, Mei  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Hjalt, Tord  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: MacDougall, John  
; APPLICANT: Stone, David  
; APPLICANT: Alsobrook II, John  
; APPLICANT: Lepley, Denise et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-416 A  
; CURRENT APPLICATION NUMBER: US/10/210,172  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/309,501  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/323,994  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/373,814  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/310,291  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 60/310,951  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/310,544  
; PRIOR FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 60/311,292  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/311,979  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 60/313,201  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/312,892  
; PRIOR FILING DATE: 2001-08-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 327  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 38  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-210-172-38

Query Match 94.9%; Score 56; DB 15; Length 711;  
Best Local Similarity 92.3%; Pred. No. 0.18;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13  
| | | | | | | | | |  
Db 591 ALAAAKAAYGAA 603

```

; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-662-10

Query Match      78.0%; Score 46; DB 10; Length 118;
Best Local Similarity 90.9%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALAAAKAAKYG 11
        | | | | | | | |
DB      40 AAAAKAAKYG 50

RESULT 10
US-09-964-662-11
; Sequence 11, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-662-11

Query Match      78.0%; Score 46; DB 10; Length 199;
Best Local Similarity 90.9%; Pred. No. 2.9;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALAAAKAAKYG 11
        | | | | | | | |
DB      39 AAAAKAAKYG 49

RESULT 11
US-09-964-662-2
; Sequence 2, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; US-10-424-599-269890
; Sequence 269890, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21153223/B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 269890
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(144)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85730C.1.pep
; US-10-424-599-269890

Query Match      83.1%; Score 49; DB 15; Length 144;
Best Local Similarity 91.7%; Pred. No. 0.59;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALAAAKAAKYGA 12
        | | | | | | | |
DB      79 AKAAAKAAKYGA 90

RESULT 8
US-09-964-662-9
; Sequence 9, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-662-9

Query Match      78.0%; Score 46; DB 10; Length 117;
Best Local Similarity 90.9%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALAAAKAAKYG 11
        | | | | | | | |
DB      39 AAAAKAAKYG 49

RESULT 9
US-09-964-662-10
; Sequence 10, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:

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; SEQ ID NO 2
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-09-964-662-2

Query Match      78.0%; Score 46; DB 10; Length 200;
Best Local Similarity 90.9%; Pred. No. 2.9;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYG 11
Db 40 AAAAAKAYG 50

RESULT 12
US-10-437-963-122700
; Sequence 122700, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122700
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25604C.1.pep
US-10-437-963-122700

Query Match      69.5%; Score 41; DB 16; Length 277;
Best Local Similarity 69.2%; Pred. No. 31;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 255 AVVAHKAASYGAA 267

RESULT 13
US-10-369-493-9086
; Sequence 9086, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9086

Query Match      69.1%; Score 39; DB 14; Length 342;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LAAAKAAYGAA 13
Db 14 LAAAKGLYGAA 25

RESULT 14
US-10-369-493-19927
; Sequence 1927, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19927
; LENGTH: 342
; TYPE: PRT
; ORGANISM: No. US20030233675Altoc punctiforme
US-10-369-493-19927

Query Match      66.1%; Score 39; DB 14; Length 342;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LAAAKAAYGAA 13
Db 14 LAAAKGLYGAA 25

RESULT 15
US-10-369-493-16900
; Sequence 16900, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16900
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-16900

Query Match      66.1%; Score 39; DB 14; Length 485;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
```

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAYG 11  
| | | | | : | |  
Db 391 ALAAANATRYG 401

RESULT 16  
US-10-078-929-116  
; Sequence 116, Application US/10078929  
; Publication No. US20020152497A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omclayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; TITLE OF INVENTION: Stress Response  
; FILE REFERENCE: B01357 US NA  
; CURRENT APPLICATION NUMBER: US/10/078, 929  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 09/566, 394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133428  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133438  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133436  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/137667  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 116  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-078-929-116

Query Match 66.1%; Score 39; DB 13; Length 569;  
Best Local Similarity 61.5%; Pred. No. 1.5e+02;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13  
| | | | | : | |  
Db 164 ALSAAKEKFGSA 176

RESULT 17  
US-10-424-599-209451  
; Sequence 209451, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 209451  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_31161C.1.pep  
US-10-424-599-209451

Query Match 64.4%; Score 38; DB 15; Length 129;  
Best Local Similarity 61.5%; Pred. No. 48;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13  
| | | | | : | |  
Db 61 AMAHLEAAKYGA 73

RESULT 18  
US-09-738-626-6936  
; Sequence 6936, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 6936  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-6936

Query Match 64.4%; Score 38; DB 9; Length 149;  
Best Local Similarity 72.7%; Pred. No. 56;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYG 11  
| | | | | : | |  
Db 38 ALATAEAAKHG 48

RESULT 19  
US-10-425-115-340008  
; Sequence 340008, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 340008  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(159)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_73254C.1.pcp  
US-10-425-115-340008

Query Match 64.4%; Score 38; DB 17; Length 159;  
Best Local Similarity 76.9%; Pred. No. 60;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
| | | | | | | | | |  
Db 100 ALAAAKAAAGAA 112

## RESULT 20

US-10-437-963-163840  
; Sequence 163840, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 163840  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_62799C.1.pcp  
US-10-437-963-163840

Query Match 64.4%; Score 38; DB 16; Length 177;  
Best Local Similarity 61.5%; Pred. No. 67;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
| | | | | | | | | |  
Db 48 ATAGKQASKYGAA 60

## RESULT 21

US-10-056-744B-4  
; Sequence 4, Application US/10056744B  
; Publication No. US20020193303A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER  
; TITLE OF INVENTION: HYDROLASE AND USES THEREFOR  
; FILE REFERENCE: MPI2001-026PIRM  
; CURRENT APPLICATION NUMBER: US/10/056,744B  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/264,167

; PRIOR FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-056-744B-4

Query Match 64.4%; Score 38; DB 13; Length 233;  
Best Local Similarity 90.0%; Pred. No. 89;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAKY 10  
| | | | | | | | | |  
Db 55 ALAAAYAAKY 64

## RESULT 22

US-10-068-134-4  
; Sequence 4, Application US/10068134  
; Publication No. US20020156264A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: 22012, A No. US20020156264A1 Human Carboxypeptidase  
; FILE REFERENCE: 5800-38  
; CURRENT APPLICATION NUMBER: US/10/068,134  
; CURRENT FILING DATE: 2002-02-06  
; PRIOR APPLICATION NUMBER: US/09/345,469  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus sequence for the alpha/beta hydrolase  
; OTHER INFORMATION: family from the Prosite database of protein  
; OTHER INFORMATION: patterns  
US-10-068-134-4

Query Match 64.4%; Score 38; DB 13; Length 251;  
Best Local Similarity 90.0%; Pred. No. 97;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAKY 10  
| | | | | | | | | |  
Db 55 ALAAAYAAKY 64

## RESULT 23

US-10-369-493-9096  
; Sequence 9096, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 9096  
; LENGTH: 463

Query Match 64.4%; Score 38; DB 13; Length 251;  
Best Local Similarity 90.0%; Pred. No. 97;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAKY 10  
| | | | | | | | | |  
Db 55 ALAAAYAAKY 64

; TYPE: PRT  
; ORGANISM: Chloroflexus aurantiacus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(463)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-9096

Query Match 64.4%; Score 38; DB 14; Length 463;  
Best Local Similarity 81.8%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYG 11  
||| ||| |||  
Db 290 ALAAAAAALYG 300

RESULT 24  
US-10-369-493-8449  
; Sequence 8449, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-21(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 8449  
; LENGTH: 482  
; TYPE: PRT  
; ORGANISM: Ralstonia metallidurans  
US-10-369-493-8449

Query Match 64.4%; Score 38; DB 14; Length 482;  
Best Local Similarity 61.5%; Pred. No. 1.9e+02;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13  
|: ||| | : |||  
Db 403 AVAAANATEYGLA 415

RESULT 25  
US-10-425-115-221398  
; Sequence 221398, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 221398  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_133506C.1.pap  
US-10-425-115-221398

Query Match 62.7%; Score 37; DB 17; Length 86;  
Best Local Similarity 58.3%; Pred. No. 48;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LAATAAKAYGAA 13  
: ||| : ||| :  
Db 12 IAASKTAQYGKA 23

## RESULT 26

US-10-425-115-353761  
; Sequence 353761, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 353761  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_85804C.1.pap  
US-10-425-115-353761

Query Match 62.7%; Score 37; DB 17; Length 152;  
Best Local Similarity 69.2%; Pred. No. 86;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13  
||| ||| |||  
Db 17 ALKVAKAVKSGAA 29

## RESULT 27

US-10-425-115-353768  
; Sequence 353768, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 353768  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_85810C.1.pap  
US-10-425-115-353768

Query Match 62.7%; Score 37; DB 17; Length 152;  
Best Local Similarity 69.2%; Pred. No. 86;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13  
||| ||| |||  
Db 17 ALKVAKAVKSGAA 29



RESULT 28  
US-10-425-115-368385  
; Sequence 368385, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 368385  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(152)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_99138C.1.pep  
US-10-425-115-368385

Query Match 62.7%; Score 37; DB 17; Length 152;  
Best Local Similarity 69.2%; Pred. No. 86;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 ALAAAKAAKYGAA 13  
||| ||| ||| |||  
Db 17 ALKVAKAVKSGAA 29

RESULT 29  
US-10-739-930-8468  
; Sequence 8468, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 8468  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(158)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: ZEAWA-23APR03-C7210\_82.p  
US-10-739-930-8468

Query Match 62.7%; Score 37; DB 17; Length 158;  
Best Local Similarity 69.2%; Pred. No. 90;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 ALAAAKAAKYGAA 13  
||| ||| ||| |||  
Db 25 ALKVAKAVKSGAA 37

RESULT 30  
US-10-425-115-353760  
; Sequence 353760, Application US/10425115  
; Publication No. US20040214272A1

; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 353760  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_85803C.1.pep  
US-10-425-115-353760

Query Match 62.7%; Score 37; DB 17; Length 177;  
Best Local Similarity 69.2%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 ALAAAKAAKYGAA 13  
||| ||| ||| |||  
Db 42 ALKVAKAVKSGAA 54

Search completed: November 19, 2004, 17:13:21  
Job time : 4.12314 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 2.65677 Seconds  
(without alignments)  
1755.321 Million cell updates/sec

Title: US-09-743-818A-13

Perfect score: 59

Sequence: 1 ALAAKAAKYGAA I3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : 1: A\_Geneseq\_23Sep04.\*

2: Geneseqp1980s.\*

3: Geneseqp1990s.\*

4: Geneseqp2000s.\*

5: Geneseqp2001s.\*

6: Geneseqp2002s.\*

7: Geneseqp2003as.\*

8: Geneseqp2003bs.\*

9: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	59	100.0	147	2	AAY01304 Human tro
2	59	100.0	171	3	AAY69137 Amino aci
3	59	100.0	183	2	AAY01311 Human tro
4	59	100.0	183	3	AAY69138 Amino aci
5	59	100.0	200	2	AAY01305 Human tro
6	59	100.0	216	2	AAY01310 Human tro
7	59	100.0	472	4	AAB88422 Human mem
8	59	100.0	617	7	ADb64761 Human pro
9	59	100.0	663	7	ADm03792 Human pro
10	59	100.0	692	7	ADb40134 Human tro
11	59	100.0	698	2	AAY01302 Human tro
12	59	100.0	698	3	AAY69069 Amino aci
13	59	100.0	712	3	AAB08630 Amino aci
14	59	100.0	730	2	AAW46315 Human ela
15	59	100.0	730	3	AAW46315 Human ela
16	59	100.0	730	5	AAO17360 Fusion pr
17	59	100.0	730	8	AAO17360 Human ela
18	59	100.0	731	3	ADq19747 Human sof
19	59	100.0	731	3	AAY69068 Amino aci
20	59	100.0	731	6	AAB66657 Human ela
21	59	100.0	731	6	ABU08725 Human ela
22	59	100.0	731	7	ADL96420 Human ela
23	59	100.0	733	2	AAB56653 Synthetic
24	59	100.0	733	2	AAY01301 Amino aci
25	59	100.0	757	7	ABg75223 Human tro
			757	7	ADP65160 Human ela

26	56	94.9	711	7	ADb40132	Human NOV
27	55	93.2	12	3	AAY69144	Peptidomi
28	55	93.2	660	2	AAY01303	Human tro
29	54	91.5	515	3	AAY69135	Amino aci
30	54	91.5	571	3	AAY69071	Amino aci
31	54	91.5	870	7	ADe08527	Novel pro
32	53	89.8	864	7	ADe56670	Rat Prote
33	51	86.4	60	2	AAY01306	Human tro
34	49	83.1	294	1	AAp82484	Tropoeias
35	46	78.0	117	4	AAB66659	MFU-3. 4/
36	46	78.0	117	6	ABU08733	Human ela
37	46	78.0	117	7	ADL96422	Human ela
38	46	78.0	118	4	AAB66660	MFU-4. 4/
39	46	78.0	118	6	ABU08734	Human ela
40	46	78.0	118	7	ADL96423	Human ela
41	46	78.0	199	4	AAB66661	MFU-5. 4/
42	46	78.0	199	6	ABU08735	Human ela
43	46	78.0	199	7	ADL96424	Human ela
44	46	78.0	200	4	AAB66658	MFU-2. 4/
45	46	78.0	200	6	ABU08726	Human ela
46	46	78.0	200	7	ADL96421	Human ela
47	46	78.0	201	2	AAW46316	Non-natur
48	43	72.9	33	8	ADP29751	Human sec
49	39	66.1	11	2	AAR04180	Monomer O
50	39	66.1	569	6	ABU58205	Rice stre
51	38	64.4	89	4	AAB79885	Corynebac
52	38	64.4	89	4	AAp79209	Corynebac
53	38	64.4	149	4	AAG93182	C glutami
54	38	64.4	233	7	ADb80253	Human 588
55	38	64.4	251	4	AAB60302	Alpha/bet
56	37	62.7	18	8	ADP29725	Human sec
57	37	62.7	25	4	AAB66787	Amphipath
58	37	62.7	84	5	ABP08143	Human ORF
59	37	62.7	122	3	AAG54636	Zea may
60	37	62.7	130	3	AAG54638	Zea may
61	37	62.7	141	8	ADN46915	Thermococ
62	37	62.7	149	3	AAG54635	Zea may
63	37	62.7	151	3	AAG40734	Zea may
64	37	62.7	152	3	AAG54637	Zea may
65	37	62.7	159	3	AAG40733	Zea may
66	37	62.7	388	4	ABb52633	Escherich
67	37	62.7	388	7	ADCO1505	Enteroha
68	37	62.7	410	5	ABb82174	C. acidov
69	37	62.7	698	7	ADc87165	Human GPC
70	37	62.7	902	6	ABU35731	Protein e
71	37	62.7	920	4	AAB66456	Protein e
72	37	62.7	920	6	ABR55195	Nucleotid
73	37	62.7	924	4	ABb67489	Drosophil
74	36	61.0	65	3	ADb01883	Streptoco
75	36	61.0	109	8	ADN47764	Thermococ
76	36	61.0	146	3	AAG35144	Arabidops
77	36	61.0	154	3	AAG29134	Arabidops
78	36	61.0	154	3	ADG09369	Arabidops
79	36	61.0	154	7	ADc87850	Ribosomal
80	36	61.0	154	7	ADc87957	Ribosomal
81	36	61.0	166	3	AAG35143	Arabidops
82	36	61.0	174	3	AAG09368	Arabidops
83	36	61.0	194	3	AAY86471	Human gen
84	36	61.0	194	6	ABO53623	Novel hum
85	36	61.0	196	6	ABU28975	Protein e
86	36	61.0	206	7	ADH86199	Enterococ
87	36	61.0	222	3	AAp90940	Cenarchae
88	36	61.0	251	7	ABO67919	Pseudomon
89	36	61.0	274	4	AAG92322	C glutami
90	36	61.0	295	3	ABY97200	Campyloba
91	36	61.0	295	6	ABJ18494	Campyloba
92	36	61.0	388	4	AAG91336	C glutami
93	36	61.0	389	8	ADJ24517	Human mod
94	36	61.0	389	8	ADN06042	Antipsori
95	36	61.0	406	4	ABb95251	Human pro
96	36	61.0	406	7	ADb60425	Human pro
97	36	61.0	406	7	ADd45850	Human pro
98	36	61.0	406	7	ADb60421	Human pro

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us-09-743-818a-13.rag

99 36 61.0 450 7 ADF05791 Agf05791 Bacterial  
100 36 61.0 489 6 ADA33347 Ada33347 Acinetoba

ALIGNMENTS

RESULT 1  
ID AAY01304 standard; protein; 147 AA.  
XX AAY01304;  
XX 07-JUN-1999 (first entry)  
XX Human tropoelastin derivative SHELgamma.  
XX  
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX WO9903886-A1.  
PN  
XX 28-JAN-1999.  
PD  
XX 17-JUL-1998; 98WO-AU000564.  
PF  
XX 18-JUL-1997; 97AU-00008117.  
PR  
XX (UNSY ) UNIV SYDNEY.  
PA  
XX Weiss AS;  
PI  
XX WPI; 1999-132162/11.  
DR N-PSDB; AAX27706.  
XX  
XX New derivatives of human tropoelastin - with elastin-like or  
PT macromolecular binding properties, useful e.g. as surgical implants.  
PT  
XX Claim 19; Fig 7; 82pp; English.  
XX  
XX The invention relates to a derivative or variant of human tropoelastin  
CC (hTE) having elastin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives  
CC or hybrid proteins containing the derivatives are useful in medical,  
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26A, from hTE. The present sequence represents a human  
CC tropoelastin derivative SHELgamma excluding the product encoded by exon  
CC 26A  
XX  
SQ Sequence 147 AA;  
Query Match 100.0%; Score 59; DB 2; Length 147;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALAAAKAAKYGAA 13  
Db 9 ALAAAKAAKYGAA 21  
RESULT 2  
AAY69137  
ID AAY69137 standard; protein; 171 AA.  
XX

AC AAY69137;  
XX 30-MAY-2000 (first entry)  
DT  
XX Amino acid sequence of a human tropoelastin derivative.  
DE  
XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
XX  
XX Homo sapiens.  
OS  
XX WO200004043-A1.  
PN  
XX 27-JAN-2000.  
PD  
XX 19-JUL-1999; 99WO-AU000580.  
PF  
XX 17-JUL-1998; 98AU-00004723.  
PR  
XX (UNSY ) UNIV SYDNEY.  
PA  
XX Weiss AS;  
PI  
XX WPI; 2000-182399/16.  
DR  
XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
PT cell growth.  
PT  
XX Disclosure; Page 133-134; 136pp; English.  
PS  
XX The present sequence represents a human tropoelastin derivative, which is  
CC representative of tropoelastin derivatives of the invention. In the  
CC tropoelastin derivatives of the invention a subsequence has been mutated  
CC so that susceptibility to proteolysis is reduced or eliminated, or a  
CC subsequence has been inserted so that susceptibility to proteolysis is  
CC increased. The derivatives have with reduced susceptibility, and can be  
CC used where the wild-type protein would be degraded too easily, e.g. in  
CC contact with serum or wound exudate. The tropoelastin derivatives provide  
CC competitive inhibition of protease activity. The tropoelastin  
CC derivatives, and other polypeptides containing tropoelastin derivative-  
CC derived protease-susceptibility sites, are useful in human or veterinary  
CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
CC and for inducing chemotaxis. They are also useful for proliferation or  
CC growth inhibition, particularly of smooth muscle cells, epithelial or  
CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
CC derivatives are competitive inhibitors of the protease, and are used for  
CC protecting against lung damage caused by elastin, for inhibiting or  
CC controlling localized growth of cancers or metastases, or to limit  
CC protease activity that causes blood clotting  
XX  
SQ Sequence 171 AA;  
Query Match 100.0%; Score 59; DB 3; Length 171;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALAAAKAAKYGAA 13  
Db 33 ALAAAKAAKYGAA 45  
RESULT 3  
AAY01311  
ID AAY01311 standard; protein; 183 AA.  
XX  
XX AAY01311;  
XX  
XX 07-JUN-1999 (first entry)  
DT  
XX Human tropoelastin derivative SHEL26-36 (excluding exon 26A product).  
DE  
XX

KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KW hand lotion; surgical implant; industrial product; human; SHEL; variant.

XX Homo sapiens.  
 OS Synthetic.

XX WO9903886-A1.

XX 28-JAN-1999.

XX 17-JUL-1998; 98WO-AU000564.

XX 18-JUL-1997; 97AU-00008117.

XX (UNSY ) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 1999-132162/11.

XX New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.

XX Claim 39; Page 11; 82pp; English.

XX The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents a human  
 CC tropoelastin derivative SHEL26-36 excluding exon 26A product

XX Sequence 183 AA;

Query Match 100.0%; Score 59; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 0.022;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13

DB 45 ALAAAKAAKYGAA 57

RESULT 4

AAAY69138

ID AAY69138 standard; protein; 183 AA.

XX AC

XX AAY69138;

XX 30-MAY-2000 (first entry)

XX Amino acid sequence of a human tropoelastin derivative.

DE

XX

XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;

XX hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;

XX Peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

XX OS

XX Homo sapiens.

XX PN

XX WO200004043-A1.

XX PD

XX 27-JAN-2000.

XX PF

XX 19-JUL-1999; 99WO-AU000580.

XX XX

XX 17-JUL-1998; 98AU-00004723.

XX

PA

XX (UNSY ) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 2000-182399/16.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.

XX PS

XX Disclosure; Page 134-135; 136pp; English.

XX CC

XX The present sequence represents a human tropoelastin derivative, which is  
 CC representative of tropoelastin derivatives of the invention. In the  
 CC tropoelastin derivatives of the invention a subsequence has been mutated  
 CC so that susceptibility to proteolysis is reduced or eliminated, or a  
 CC subsequence has been inserted so that susceptibility to proteolysis is  
 CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary  
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
 CC and for inducing chemotaxis. They are also useful for proliferation or  
 CC growth inhibition, particularly of smooth muscle cells, epithelial or  
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
 CC derivatives are competitive inhibitors of the protease, and are used for  
 CC protecting against lung damage caused by elastin, for inhibiting or  
 CC controlling localized growth of cancers or metastases, or to limit  
 CC protease activity that causes blood clotting

XX SQ

XX Sequence 183 AA;

Query Match 100.0%; Score 59; DB 3; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13

DB 45 ALAAAKAAKYGAA 57

RESULT 5

AAAY01305

ID AAY01305 standard; protein; 200 AA.

XX AC

XX AAY01305;

XX 07-JUN-1999 (first entry)

XX DE

XX Human tropoelastin derivative SHELgamma.

XX KW

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;

XX pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;

XX hand lotion; surgical implant; industrial product; human; SHEL; variant.

XX OS

XX Homo sapiens.

XX OS

XX Synthetic.

XX PN

XX WO9903886-A1.

XX XX

XX 28-JAN-1999.

XX PF

XX 17-JUL-1998; 98WO-AU000564.

XX PR

XX 18-JUL-1997; 97AU-00008117.

XX PA

XX (UNSY ) UNIV SYDNEY.

XX Weiss AS;

XX XX



CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA) Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes

XX Sequence 472 AA;  
 SQ

Query Match 100.0%; Score 59; DB 4; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 0.06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 Db 360 ALAAAKAAKYGAA 372

RESULT 8  
 ADB64761  
 ID ADB64761 standard; protein; 617 AA.  
 XX  
 AC ADB64761;  
 XX  
 DT 04-DEC-2003 (first entry)  
 DE Human protein encoded by clone NT2RP70003110.  
 XX  
 KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;  
 KW cell regeneration; membrane protein; signal transduction-related protein;  
 KW transcription-related protein; osteoporosis; neurological disease;  
 KW cancer; tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1308459-A2.  
 XX  
 PD 07-MAY-2003.  
 XX  
 PF 28-MAR-2002; 2002EP-00007401.  
 XX  
 PR 05-NOV-2001; 2001JP-00373298.  
 PR 25-JAN-2002; 2002US-00350978.  
 XX  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX WPI; 2003-450961/43.  
 DR N-PSDB; ADB62791.  
 XX  
 PT New polynucleotides and polypeptides, useful for developing a diagnostic  
 PT marker or medicines for regulation of their expression and activity, or  
 PT as targets of gene therapy.  
 XX  
 PS Claim 1; Page; 22pp; English.  
 XX  
 CC The invention discloses a polynucleotide comprising a sequence selected  
 CC from 1970 fully defined nucleotide sequences which encode novel  
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
 CC or its partial peptide, an antibody binding to the polypeptide or peptide  
 CC of the polynucleotide, immunologically assaying the polypeptide or  
 CC peptide of the polynucleotide by contacting the polypeptide or peptide  
 CC with the antibody of the encoded protein, and observing the binding  
 CC between the two, a transformant carrying the polynucleotide in an  
 CC expressible manner and an antisense polynucleotide. The oligonucleotide  
 CC is useful as a primer for synthesizing the polynucleotide, or as a probe  
 CC for detecting the polynucleotide. The polynucleotides and encoded  
 CC proteins are useful as pharmaceutical agents and many disease-related  
 CC genes may be included in them, for developing a diagnostic marker or

CC medicines for regulation of their expression and activity, or as targets  
 CC of gene therapy. The genes are involved in tissue and/or cell  
 CC regeneration. Membrane proteins, signal transduction-related proteins,  
 CC transcription-related proteins, disease-related proteins and genes  
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate  
 CC the activity or expression of the encoded protein to treat diseases. The  
 CC sequence presented is a protein of the invention. Note: Some of the  
 CC sequence data for this patent is not represented in the printed  
 CC specification, but is based on sequence information supplied by the  
 CC European Patent Office.  
 XX Sequence 617 AA;  
 SQ

Query Match 100.0%; Score 59; DB 7; Length 617;  
 Best Local Similarity 100.0%; Pred. No. 0.08; Mismatches 0; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 Db 497 ALAAAKAAKYGAA 509

RESULT 9  
 ADM03792  
 ID ADM03792 standard; protein; 563 AA.  
 XX  
 AC ADM03792;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human protein of the invention SEQ ID NO:2477.  
 XX  
 KW human; gene therapy; diagnostic marker; pharmaceutical.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1347046-A1.  
 XX  
 PD 24-SEP-2003.  
 XX  
 PF 12-APR-2002; 2002EP-00008400.  
 XX  
 PR 22-MAR-2002; 2002JP-00137785.  
 XX  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX WPI; 2003-723558/69.  
 DR N-PSDB; ADM01349.  
 XX  
 PT New polynucleotides and polypeptides are useful in gene therapy, for  
 PT developing a diagnostic marker or medicines for regulating their  
 PT expression and activity, or as a target of gene therapy.  
 XX  
 PS Claim 1; SEQ ID NO 2477; 305pp; English.  
 XX  
 CC The invention relates to a novel human polynucleotide and the encoded  
 CC polypeptide. A polynucleotide of the invention may have a use in gene  
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
 CC as a primer for synthesizing the polynucleotide or as a probe for  
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM01758 are  
 CC useful in gene therapy, for developing a diagnostic marker or medicines  
 CC for regulating their expression and activity, or as a target of gene  
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
 CC are useful as pharmaceutical agents. The present sequence represents a  
 CC protein sequence of the invention.  
 XX Sequence 663 AA;  
 SQ

Query Match 100.0%; Score 59; DB 7; Length 663;  
 Best Local Similarity 100.0%; Pred. No. 0.086;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 Db 525 ALAAAKAAKYGAA 537

RESULT 10  
 ADE40134  
 ID ADE40134 standard; protein; 692 AA.  
 XX AC  
 AC ADE40134;  
 XX AC  
 DT 29-JAN-2004 (first entry)  
 DE Human NOV16b protein - SEQ ID 40.  
 XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
 KW anti-diabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
 KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;  
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
 KW aschma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
 KW tissue typing; human; NOV.  
 XX OS  
 OS Homo sapiens.  
 XX WO2003064589-A2.  
 XX 07-AUG-2003.  
 XX 02-AUG-2002; 2002WO-US024483.  
 XX 02-AUG-2001; 2001US-0309501P.  
 XX 03-AUG-2001; 2001US-0310291P.  
 XX 07-AUG-2001; 2001US-0310544P.  
 XX 08-AUG-2001; 2001US-0310951P.  
 XX 09-AUG-2001; 2001US-0311292P.  
 XX 13-AUG-2001; 2001US-0311979P.  
 XX 16-AUG-2001; 2001US-0312892P.  
 XX 17-AUG-2001; 2001US-0313201P.  
 XX 17-AUG-2001; 2001US-0313415P.  
 XX 20-AUG-2001; 2001US-0313643P.  
 XX 20-AUG-2001; 2001US-0313702P.  
 XX 21-AUG-2001; 2001US-0314031P.  
 XX 23-AUG-2001; 2001US-0314466P.  
 XX 28-AUG-2001; 2001US-0315403P.  
 XX 29-AUG-2001; 2001US-0315853P.  
 XX 17-SEP-2001; 2001US-0322716P.  
 XX 21-SEP-2001; 2001US-0323994P.  
 XX 14-DEC-2001; 2001US-0340233P.  
 XX 05-FEB-2002; 2002US-0354591P.  
 XX 19-MAR-2002; 2002US-0365478P.  
 XX 19-APR-2002; 2002US-0373814P.  
 XX 19-APR-2002; 2002US-0373825P.  
 XX 19-APR-2002; 2002US-0373989P.  
 XX 23-APR-2002; 2002US-0374632P.  
 XX 07-JUN-2002; 2002US-0386971P.  
 XX 01-AUG-2002; 2002US-00210172.  
 XX (CURA-) CURAGEN CORP.  
 XX Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;  
 PI Shimkets RA, Zerhusen BD, Li L, Padigaru M, Casman SJ;  
 PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;  
 PI Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;  
 PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DU;  
 PI Alsobrook JF, Lepley DM, Burgess CE, Majumder K, Wolenc AR,  
 PI Smithson G;  
 XX WPI; 2003-663472/62.

DR N-PSDB; ADE40133.  
 XX New NOVX polypeptides and nucleic acids, useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX XX  
 PS Claim 1; SEQ ID NO 40; 560pp; English.  
 XX The invention relates to a novel NOVX polypeptide. The polypeptide of the  
 CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,  
 CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
 CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and  
 CC gynaecological activities and may be useful in diagnosing, treating or  
 CC preventing NOVX-associated disorders including cardiomyopathy,  
 CC atherosclerosis, hypertension, cancer, obesity, diabetes, Parkinson's  
 CC sclerosis, graft-versus-host disease, Alzheimer's disease, multiple  
 CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
 CC be utilised as vaccines whilst the nucleic acids may be used as  
 CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
 CC preventive medicine and pharmacogenomics. The current sequence is that of  
 CC the human NOV protein of the invention.  
 XX Sequence 692 AA;  
 SQ Query Match 100.0%; Score 59; DB 7; Length 692;  
 Best Local Similarity 100.0%; Pred. No. 0.09;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 Db 554 ALAAAKAAKYGAA 566

RESULT 11  
 AAY01302  
 ID AAY01302 standard; protein; 698 AA.  
 XX AC  
 AC AAY01302;  
 XX 07-JUN-1999 (first entry)  
 XX Human tropoelastin variant SHELdelta26A.  
 XX KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX WO9903886-A1.  
 XX 28-JAN-1999.  
 XX 17-JUL-1998; 98WO-AU000564.  
 XX 18-JUL-1997; 97AU-00008117.  
 XX (UNSY) UNIV SYDNEY.  
 XX Weiss AS;  
 XX WPI; 1999-132162/11.  
 XX New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.  
 XX Claim 13; Fig 2; 82pp; English.  
 XX The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG)) -binding properties. Cells containing vectors



CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents the synthetic  
 CC human tropoelastin variant SHELDelta26A  
 XX  
 SQ Sequence 698 AA;

Query Match 100.0%; Score 59; DB 2; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 0.091;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 Db 560 ALAAAKAAKYGAA 572

RESULT 12  
 AAY69069  
 ID AAY69069 standard; protein; 698 AA.  
 AC  
 XX AAY69069;

DT 30-MAY-2000 (first entry)  
 DE Amino acid sequence of a human reduced tropoelastin derivative.

CC Tropoelastin; derivative; SHELDelta-26a; SHEL; proteolysis; protease;  
 CC antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;  
 CC growth inhibition; peptidomimetic; lung damage; elastin; cancer;  
 CC metastasis; blood clotting.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.

XX WO200004043-A1.  
 PN  
 XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-AU000580.  
 PF  
 XX 17-JUL-1998; 98AU-00004723.

XX (UNSY ) UNIV SYDNEY.  
 XX Weiss AS;  
 XX WPI; 2000-182399/16.  
 DR N-PSDB; AAZ61144.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 XX cell growth.  
 XX  
 PS Disclosure; Page 110-112; 136pp; English.

CC The present sequence represents a human reduced tropoelastin derivative,  
 CC designated SHELDelta-26a. The sequence is produced by removing exon 26a  
 CC of SHEL (SHEL not defined). The protein is representative of tropoelastin  
 CC derivatives of the invention, in which a subsequence has been mutated so  
 CC that susceptibility to proteolysis is reduced or eliminated, or a  
 CC subsequence has been inserted so that susceptibility to proteolysis is  
 CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary  
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
 CC and for inducing chemotaxis. They are also useful for proliferation or

CC growth inhibition, particularly of smooth muscle cells, epithelial or  
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
 CC derivatives are competitive inhibitors of the protease, and are used for  
 CC protecting against lung damage caused by elastin, for inhibiting or  
 CC controlling localized growth of cancers or metastases, or to limit  
 CC protease activity that causes blood clotting  
 XX  
 SQ Sequence 698 AA;

Query Match 100.0%; Score 59; DB 3; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 0.091;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 Db 560 ALAAAKAAKYGAA 572

RESULT 13  
 AAB08630  
 ID AAB08630 standard; peptide; 712 AA.  
 XX  
 AC AAB08630;

XX 20-DEC-2000 (first entry)  
 DT  
 DE Amino acid sequence of a human elastin polypeptide.

CC Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;  
 CC smooth muscle cell differentiation; smooth muscle cell migration;  
 CC smooth muscle cell function; atherosclerosis; restenosis; aneurysm;  
 CC vascular bypass graft stenosis; transplant arteriopathy; dissection;  
 CC SVAS; hypertension; transplant arteriopathy.  
 XX  
 OS Homo sapiens.

XX WO2000050068-A2.  
 PN  
 XX 31-AUG-2000.

XX 28-FEB-2000; 2000WO-US002526.  
 PF  
 XX 26-FEB-1999; 99US-00258217.

XX (UTAH ) UNIV UTAH RES FOUND.  
 XX Keating MT, Li DY;  
 XX WPI; 2000-533134/48.

XX Elastin based compositions useful for treating atherosclerosis,  
 XX restenosis, vascular bypass graft stenosis, transplant arteriopathy,  
 XX aneurysm, dissection SVAS and/or hypertension.  
 XX  
 PS Example 3; Page 46; 79pp; English.

CC The present sequence represents a human elastin. Peptides derived from  
 CC elastin are used in compositions of the invention. The specification  
 CC describes elastin based compositions that are potent regulators of smooth  
 CC muscle cell proliferation, differentiation and migration in vivo. The  
 CC elastin-based compositions comprise at least one elastic fibre, elastins,  
 CC tropoelastins (or fragments of them) which have biological activities  
 CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;  
 CC stimulating the differentiation of smooth muscle cells in vivo;  
 CC regulating the migration of smooth muscle cells in vivo; and  
 CC may be used for the prophylaxis or treatment of a disorder characterized  
 CC by diminished capacity to regulate smooth muscle cell function such as  
 CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant  
 CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated  
 CC also include SVAS (undefined), hypertension, and transplant arteriopathy  
 XX  
 SQ Sequence 712 AA;

```
XX SQ Sequence 730 AA;
Query Match 100.0%; Score 59; DB 3; Length 712;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
| | | | | | | | | |
Db 592 ALAAAKAAYGAA 604

RESULT 14
AAW46315
ID AAW46315 standard; protein; 730 AA.
XX
AC AAW46315;
XX
DT 23-JUL-1998 (first entry)
XX
DE Human elastin containing non-natural polypeptide MFU-1 sequence.
XX
KW MFU-1; minimal functional unit; elastin; human; fibrous protein;
KW beta-sheet; coating; wound dressing.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 374..499
FT /note= "MFU-1 polypeptide"
XX
PN WO9805685-A2.
XX
PD 12-FEB-1998.
XX
PE 07-AUG-1997; 97WO-CA000560.
XX
PR 07-AUG-1996; 96US-0023552P.
PR 07-AUG-1997; 97US-00911364.
XX
PA (PROT-) PROTEIN SPECIALTIES LTD.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI Rothstein A, Keeley FW, Rothstein SJ;
XX
XX MPI; 1998-145551/13.
XX
XX New non-natural polypeptide with multiple beta-sheet, beta-turn
PT structures - particularly based on human elastin, useful for coating
PT prostheses, as wound dressings, etc., allows ingrowth of cells.
XX
PS Claim 5; Fig 1B; 39pp; English.
XX
XX This represents the human elastin sequence containing the minimal
CC functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a
CC polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is
CC not a naturally occurring fibrous protein. Each beta-sheet structure has
CC 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at
CC least 1 amino acid that can take part in crosslinking. The polypeptide
CC can also be derived from the sequences of animal elastin, lamprin and
CC spider silk protein. The MFU polypeptides are self-aligning peptides
CC having the same primary structure as part of a natural fibrous protein.
CC They are used to coat prostheses made of animal or synthetic material or
CC metal, particularly for use as blood vessel or heart valve replacements,
CC wound or burn dressings, or stents. They can be used in cosmetic, elastic
CC or high-tensile strength materials, e.g. ropes or parachute cord,
CC prostheses based on the MFU allow penetration of endothelial cells, so
CC become permanent, living, tissue replacements. The MFU polypeptides have
CC better biocompatibility than known elastin-based materials. They are well
CC defined, homogeneous material and are easier to manipulate and produce
CC than full-length elastins. They are non-thrombogenic and non-immunogenic.
CC Materials can be made from 2 or more different MFU polypeptides to allow
CC properties to be tailored for particular applications, e.g. combining the
CC high extensibility of elastin and the high tensile strength of spider
CC silk protein
```

```
XX SQ Sequence 730 AA;
Query Match 100.0%; Score 59; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
| | | | | | | | | |
Db 593 ALAAAKAAYGAA 605

RESULT 15
AAB08631
ID AAB08631 standard; peptide; 730 AA.
XX
AC AAB08631;
XX
DT 20-DEC-2000 (first entry)
XX
DE Fusion protein comprising human elastin and c-myc.
XX
KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW smooth muscle cell differentiation; smooth muscle cell migration;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW SVAS; hypertension; transplant arteriopathy.
XX
OS Synthetic.
OS Homo sapiens.
OS Unidentified.
XX
PN WO200050068-A2.
XX
PD 31-AUG-2000.
XX
PE 28-FEB-2000; 2000WO-US002526.
XX
PR 26-FEB-1999; 99US-00258217.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Keating MT, Li DY;
XX
XX MPI; 2000-533134/48.
XX
XX Elastin based compositions useful for treating atherosclerosis,
PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
PT aneurysm, dissection SVAS and/or hypertension.
XX
PS Example 3; Page 48; 79pp; English.
XX
XX The present sequence represents a fusion protein, comprising human
CC elastin and c-myc, preceded by a His tag. The protein is used in
CC compositions of the invention. The specification describes elastin based
CC compositions that are potent regulators of smooth muscle cell
CC proliferation, differentiation and migration in vivo. The elastin-based
CC compositions comprise at least one elastic fibre, elastins, tropoelastins
CC (or fragments of them) which have biological activities comprising:
CC inhibiting the proliferation of smooth muscle cells in vivo; stimulating
CC the differentiation of smooth muscle cell in vivo; and regulating the
CC migration of smooth muscle cells in vivo. The compositions may be used
CC for the prophylaxis or treatment of a disorder characterized by
CC diminished capacity to regulate smooth muscle cell function such as
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
CC arteriopathy aneurysm and/or dissection. Disorders which may be treated
CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX
XX Sequence 730 AA;
Query Match 100.0%; Score 59; DB 3; Length 730;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 ALAAAKAAKYGAA 13  
 DB 601 ALAAAKAAKYGAA 613

RESULT 16  
 ID AAO17360  
 AC AAO17360 standard; protein; 730 AA.  
 XX AAO17360;  
 XX 19-JUL-2002 (first entry)  
 XX Human elastin.  
 XX Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;  
 KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;  
 KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;  
 KW transmembrane receptor PTK7; collagen type XVIII alpha 1;  
 KW platelet derived growth factor receptor alpha; laminin M chain;  
 KW subtilisin like protein PACE4; nidogen.  
 XX  
 OS Homo sapiens.  
 XX  
 XX EP1191107-A2.  
 XX 27-MAR-2002.  
 XX 21-AUG-2001; 2001EP-00250300.  
 XX 25-SEP-2000; 2000DE-01048633.  
 XX (SCHD ) SCHERING AG.  
 XX Hess-Stumpp H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;  
 PI Regidor P, Scotti S;  
 XX WPI; 2002-317413/36.  
 XX  
 XX In vitro diagnosis and monitoring of endometriosis, comprises detecting  
 PT reduced expression of specific gene products, e.g. from the fibronectin  
 PT gene.  
 XX Claim 1; Page 15-16; 21pp; German.  
 XX  
 CC The present invention relates to a method for the in vitro diagnosis of  
 CC endometriosis by determining the amount of gene product from at least one  
 CC specific gene in a patient sample and comparing this with the amount of  
 CC gene product in a control sample. A reduced level is indicative of  
 CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,  
 CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,  
 CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,  
 CC transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet  
 CC derived growth factor receptor alpha, laminin M chain, subtilisin like  
 CC protein PACE4 or nidogen. The method is useful for initial diagnosis of  
 CC endometriosis, and also for monitoring progress and treatment of the  
 CC disease. The present sequence is human elastin  
 XX  
 XX Sequence 730 AA;  
 XX  
 Query Match 100.0%; Score 59; DB 5; Length 730;  
 Best Local Similarity 100.0%; Pred. No. 0.095;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALAAAKAAKYGAA 13  
 DB 592 ALAAAKAAKYGAA 604

RESULT 17  
 ID ADQ19747  
 AC ADQ19747 standard; protein; 730 AA.

XX ADQ19747;  
 XX 26-AUG-2004 (first entry)  
 XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.  
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.  
 XX Homo sapiens.  
 XX WO2004048938-A2.  
 XX 10-JUN-2004.  
 XX 26-NOV-2003; 2003WO-US038193.  
 XX 26-NOV-2002; 2002US-0429739P.  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 XX Aziz N, Ginsburg WM, Zlotnik A;  
 XX WPI; 2004-441208/41.  
 XX Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 XX  
 XX Example 2; SEQ ID NO 2566; 210pp; English.  
 XX  
 CC The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytostatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 CC acid sequences may be useful in diagnostic and screening applications.  
 CC The current sequence is that of a human soft tissue sarcoma-upregulated  
 CC protein of the invention. The current sequence is not shown within the  
 CC specification per se but was submitted in CD format by the inventor.  
 XX  
 XX Sequence 730 AA;  
 XX  
 Query Match 100.0%; Score 59; DB 8; Length 730;  
 Best Local Similarity 100.0%; Pred. No. 0.095;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALAAAKAAKYGAA 13  
 DB 592 ALAAAKAAKYGAA 604

RESULT 18  
 ID AAY69068  
 AC AAY69068 standard; protein; 731 AA.  
 XX AAY69068;  
 XX 30-MAY-2000 (first entry)  
 XX Amino acid sequence of a human tropoelastin splice form.  
 XX  
 XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX Homo sapiens.  
 XX

EH	Key	Location/Qualifiers	PD	04-JAN-2001.
FT	Cleavage-site	441..442	XX	
FT	Cleavage-site	503..504	XX	29-JUN-2000; 2000WO-US017829.
FT	Cleavage-site	515..516	XX	
FT	Cleavage-site	564..565	XX	29-JUN-1999; 99US-00340736.
XX			XX	(PROT-) PROTEIN SPECIALTIES LTD.
PN	WO200004043-A1.		PA	(HSCR-) HSC RES & DEV LP.
XX			XX	
XX	27-JAN-2000.		PI	Rothstein A, Keeley F, Rothstein S, Stahl R;
XX			XX	WPI; 2001-102886/11.
XX	19-JUL-1999; 99WO-AU000580.		DR	
XX			XX	
XX	17-JUL-1998; 98AU-00004723.		XX	
XX			PT	Novel polypeptides that comprise three beta-sheet/beta-turn structures
XX	(UNSY ) UNIV SYDNEY.		PT	and are not naturally occurring fibrous protein, used to produce
PA			PT	prosthesis suitable for implantation into humans, and cosmetic materials.
XX	Weiss AS;		XX	
XX			PS	Claim 1; Fig 1; 39pp; English.
XX			XX	
XX	WPI; 2000-182399/16.		XX	
DR	N-ESDB; AAZ61146.		CC	The present invention relates to a minimal functional unit (MFU) of human
XX			CC	elastin polypeptide. This protein is useful in a cosmetic material or a
XX			CC	prosthetic material such as prosthesis for blood vessel replacements, for
XX	New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and		CC	heart valve replacement, tissue replacement, for covering burns, for
PT	cell growth.		CC	covering wounds and stents
XX			XX	
XX	Disclosure; Page 107-109; 136pp; English.		XX	
XX			SQ	Sequence 731 AA;
CC	The present sequence represents a human tropoelastin splice form. The			
CC	specification describes tropoelastin derivatives, in which a subsequence			
CC	has been mutated so that susceptibility to proteolysis is reduced or			
CC	eliminated, or a subsequence has been inserted so that susceptibility to			
CC	proteolysis is increased. The derivatives have with reduced			
CC	susceptibility, and can be used where the wild-type protein would be			
CC	degraded too easily, e.g. in contact with serum or wound exudate. The			
CC	tropoelastin derivatives provide competitive inhibition of protease			
CC	activity. The tropoelastin derivatives, and other polypeptides containing			
CC	tropoelastin derivative-derived protease-susceptibility sites, are useful			
CC	in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand			
CC	lotions), as bulking agents and for inducing chemotaxis. They are also			
CC	useful for proliferation or growth inhibition, particularly of smooth			
CC	muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,			
CC	chondrocytes and platelets. Peptidomimetics that mimic the protease			
CC	cleavage site in tropoelastin derivatives are competitive inhibitors of			
CC	the protease, and are used for protecting against lung damage caused by			
CC	elastin, for inhibiting or controlling localized growth of cancers or			
CC	metastases, or to limit protease activity that causes blood clotting			
XX				
SQ	Sequence 731 AA;			
	Query Match	100.0%; Score 59; DB 3; Length 731;		
	Best Local Similarity	100.0%; Pred. No. 0.096;		
	Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	1 ALAAAKAAKYGAA 13			
Db	593 ALAAAKAAKYGAA 605			
RESULT 19				
AAB66657				
ID	AAB66657 standard; protein; 731 AA.			
XX				
AC	AAB66657;			
XX				
DT	05-APR-2001 (first entry)			
XX				
DE	Human elastin protein without signal peptide.			
XX				
KW	Minimal function unit; MFU; human; elastin prosthetic.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200100666-A2.			
XX				
	Query Match	100.0%; Score 59; DB 3; Length 731;		
	Best Local Similarity	100.0%; Pred. No. 0.096;		
	Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	1 ALAAAKAAKYGAA 13			
Db	593 ALAAAKAAKYGAA 605			
RESULT 19				
AAB66657				
ID	AAB66657 standard; protein; 731 AA.			
XX				
AC	AAB66657;			
XX				
DT	05-APR-2001 (first entry)			
XX				
DE	Human elastin protein without signal peptide.			
XX				
KW	Minimal function unit; MFU; human; elastin prosthetic.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200100666-A2.			
XX				
	Query Match	100.0%; Score 59; DB 4; Length 731;		
	Best Local Similarity	100.0%; Pred. No. 0.096;		
	Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	1 ALAAAKAAKYGAA 13			
Db	593 ALAAAKAAKYGAA 605			
RESULT 20				
ABU08725				
ID	ABU08725 standard; protein; 731 AA.			
XX				
AC	ABU08725;			
XX				
DT	25-JUN-2003 (first entry)			
XX				
DE	Human elastin mature protein.			
XX				
KW	Human; elastin; minimal functioning unit; MFU;			
KW	beta-sheet/beta-turn structure; fibrous protein; prosthesis;			
KW	blood vessel replacement; heart replacement valve; burn; wound; lamprin;			
KW	spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;			
KW	platelet activation inhibitor; non-thrombogenic; cell infiltration;			
KW	non-immunogenic; biocompatible; high tensile strength; elasticity;			
KW	plasticity.			
XX				
OS	Homo sapiens.			
XX				
PN	US6489446-B1.			
XX				
PD	03-DEC-2002.			
XX				
PF	29-JUN-1999; 99US-00340736.			
XX				
PR	07-AUG-1996; 96US-0023522P.			
XX				
PR	07-AUG-1997; 97US-00911364.			
XX				
PA	(HSCR-) HSC RES & DEV LP.			
XX				
PA	(PROT-) PROTEIN SPECIALTIES LTD.			
XX				
PI	Rothstein A, Keeley F, Rothstein S;			
XX				
DR	WPI; 2003-391056/37.			
XX				
PT	Novel polypeptide useful in prosthesis, has a secondary structure			

PT characterized by three beta-sheet/beta-turn structures, and is not a  
 XX naturally occurring fibrous protein.

XX Claim 1; Fig 1B; 21pp; English.

XX The invention describes a polypeptide (I) comprising a minimal  
 CC functioning unit (MFU) which is present in the sequence of human elastin  
 CC and comprised of at least three beta-sheet/beta-turn structures, and at  
 CC least one amino acid residue that participates in cross-linking, and not  
 CC a naturally occurring fibrous protein. The MFU material can be used to  
 CC construct human elastin-like prostheses such as tubes for blood vessel  
 CC replacement, heart replacement valves and sheets for other uses such as  
 CC burns or wounds to promote healing. MFUs can be co-aggregated with other  
 CC proteins, for e.g. collagen, to provide prostheses material that  
 CC resembles the natural structural materials of the body. MFUs modeled on  
 CC lamprin and other fibrous proteins e.g. spider silk, can be used to make  
 CC a variety of materials, for a number of different applications, for e.g.  
 CC in cords and ropes for use in parachutes and in cosmetics. Coating  
 CC synthetic prostheses with MFUs modeled on human elastin significantly  
 CC inhibits platelet binding and activation. The human-like MFU material is  
 CC more biocompatible than other elastin-containing materials. In contrast  
 CC to solubilised fragments of elastin used before, an MFU is a single  
 CC peptide of defined composition. The MFU is considerably smaller than the  
 CC parent protein, simpler in structure, easier to produce or express in  
 CC quantity, to handle in solution and to manipulate for experimental and  
 CC practical purposes. Like other elastin preparations, the MFU is non-  
 CC thrombogenic and provides a friendly environment for cell infiltration.  
 CC Being composed entirely of a human elastin sequence, MFU is non-  
 CC immunogenic, thus providing a truly biocompatible material. MFUs modeled  
 CC on lamprin and other fibrous proteins can be used to make a variety of  
 CC materials having high tensile strength, elasticity and plasticity of  
 CC their parent proteins. This is the amino acid sequence of mature human  
 CC elastin on which the MFU peptides of the invention are based

XX Sequence 731 AA;

Query Match 100.0%; Score 59; DB 6; Length 731;  
 Best Local Similarity 100.0%; Pred. No. 0.096;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 Db 593 ALAAAKAAKYGAA 605

RESULT 21  
 ADL96420

ID ADL96420 standard; protein; 731 AA.

XX AC ADL96420;

XX 20-MAY-2004 (first entry)

XX Human elastin protein fragment.

XX fibrous protein; prosthesis; elastin; lamprin; spider silk protein;  
 XX blood vessel; wound; burn healing; collagen.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Region 19..160

FT /note= "region specifically claimed in claim 6"

FT Region 188..367

FT /note= "region specifically claimed in claim 6"

FT Region 374..499

FT /note= "region specifically claimed in claim 6"

FT Region 607..717

FT /note= "region specifically claimed in claim 6"

XX US2003166846-A1.

XX 04-SEP-2003.

XX 28-SEP-2001; 2001US-00964662.

XX 07-AUG-1996; 96US-0023522P.

XX 07-AUG-1997; 97US-00911364.

XX 29-JUN-1999; 99US-00340736.

XX (ROTH/) ROTHSTEIN A.

XX (KEEL/) KEELEY F.

XX (ROTH/) ROTHSTEIN S.

XX Rothstein A, Keeley F, Rothstein S;

XX WPI; 2003-898105/82.

XX Polypeptide for constructing human elastin-like prostheses such as tubes  
 PT for blood vessel replacement and sheets for other uses such as wound or  
 PT burn healing, comprises three beta sheets and three beta turns.

XX Claim 5; Fig 1B; 17pp; English.

XX This invention describes a polypeptide that comprises three beta  
 CC sheet/beta turn structures and that is not a naturally occurring fibrous  
 CC protein. The invention also describes a prosthesis comprising an animal,  
 CC metal or synthetic material, where the surface is coated with the  
 CC polypeptide, a cosmetic material comprising the polypeptide, an elastic  
 CC material comprising the polypeptide, a high tensile strength material  
 CC comprising the polypeptide, a material comprising two or more  
 CC polypeptides selected from (a) a polypeptide consisting essentially of a  
 CC portion of the polypeptide comprising at least three beta sheet/beta turn  
 CC structures, (b) a polypeptide consisting essentially of a portion of the  
 CC amino acid sequence of an animal elastin comprising at least three beta  
 CC sheets/beta turns, (c) a polypeptide consisting essentially of a portion  
 CC of lamprin comprising at least three beta sheets/beta turns, and (d) a  
 CC polypeptide consisting essentially of a spider silk protein comprising at  
 CC least three beta sheets/beta turns, a polypeptide having the primary  
 CC structure of a portion of a naturally occurring fibrous protein and a  
 CC secondary structure comprising at least three beta sheets/beta turns,  
 CC where each of the beta sheet/beta turn structures comprises from 3 to  
 CC about 7 amino acids and the polypeptide is not a naturally occurring  
 CC fibrous protein. The minimal functional unit (MFU) of the invention is  
 CC useful to construct human elastin-like prostheses such as tubes for blood  
 CC vessel replacement and sheets for other uses such as wound or burn  
 CC healing. Alternatively the MFU can be co-aggregated with other proteins,  
 CC for example collagen, to provide prostheses material that resembles the  
 CC natural structural materials of the body. The MFU based material is  
 CC subject to infiltration of cells growing in the patient, including  
 CC endothelial cells, and the prosthesis can become a permanent living  
 CC tissue replacement. The material is more biocompatible than other elastin  
 CC -containing materials proposed for prostheses.

XX Sequence 731 AA;

Query Match 100.0%; Score 59; DB 7; Length 731;  
 Best Local Similarity 100.0%; Pred. No. 0.096;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 Db 593 ALAAAKAAKYGAA 605

RESULT 22

AAR56653

ID AAR56653 standard; protein; 733 AA.

XX AC AAR56653;

XX 25-MAR-2003 (revised)

XX 22-MAR-1995 (first entry)

XX Synthetic human tropoelastin (SHEL).

KW Tropoelastin; pharmaceutical; surgical dressing.  
 XX Synthetic.  
 OS  
 XX WO9414958-A1.  
 PN  
 XX 07-JUL-1994.  
 PD  
 XX 16-DEC-1993; 93WO-AU0000655.  
 XX  
 XX 22-DEC-1992; 92AU-00006520.  
 PR  
 XX 28-JUN-1993; 93AU-00009661.  
 PR  
 XX (UNSY ) UNIV SYDNEY.  
 PA  
 PI Weiss AS, Martin SL;  
 XX  
 XX WPI; 1994-263633/32.  
 XX  
 DR N-PSDB; AAQ70941.  
 DR  
 XX Synthetic polynucleotide(s) - encode recombinant tropoelastins and  
 PT variants.  
 XX  
 PS Disclosure; Page 30; 77pp; English.  
 XX  
 XX Human synthetic tropoelastin is susceptible to hydrolytic breakdown of  
 CC the crosslinks. Such material may be useful in e.g. surgical  
 CC applications, where the gradual loss of material over time is intended.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 733 AA;  
 SQ

Query Match 100.0%; Score 59; DB 2; Length 733;  
 Best Local Similarity 100.0%; Pred. No. 0.096;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 DB 595 ALAAAKAAKYGAA 607  
 |||||

RESULT 23  
 AAY01301  
 ID AAY01301 standard; protein; 733 AA.  
 XX  
 AC AAY01301;  
 XX  
 DT 07-JUN-1999 (first entry)  
 XX  
 DE Amino acid sequence of synthetic human tropoelastin SHEL.  
 XX  
 XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KW hand lotion; surgical implant; industrial product; human; SHEL.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9903886-A1.  
 PN  
 PD 28-JAN-1999.  
 XX  
 XX 17-JUL-1998; 98WO-AU0000564.  
 PF  
 XX 18-JUL-1997; 97AU-00008117.  
 PR  
 XX (UNSY ) UNIV SYDNEY.  
 PA  
 XX Weiss AS;  
 PI  
 XX WPI; 1999-132162/11.  
 DR  
 DR N-PSDB; AAX27704.  
 XX

PT New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.  
 XX  
 XX Disclosure; Fig 1; 82pp; English.  
 PS  
 XX The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents the amino acid  
 CC sequence of the synthetic human tropoelastin SHEL  
 XX  
 SQ Sequence 733 AA;  
 Query Match 100.0%; Score 59; DB 2; Length 733;  
 Best Local Similarity 100.0%; Pred. No. 0.096;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13  
 |||||  
 DB 595 ALAAAKAAKYGAA 607  
 |||||

RESULT 24  
 ABG75223  
 ID ABG75223 standard; protein; 757 AA.  
 XX  
 AC ABG75223;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human tropoelastin protein.  
 XX  
 XX Human; tropoelastin; elastin; body vessel occlusion; stenosis;  
 KW vascular smooth muscle cell; elastin signaling; vasotrophic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003082203-A2.  
 PN  
 XX 09-OCT-2003.  
 PD  
 XX 27-MAR-2003; 2003WO-US009391.  
 PF  
 XX 27-MAR-2002; 2002US-0368084P.  
 PR  
 XX (UTAH ) UNIV UTAH RES FOUND.  
 PA  
 XX Li DY, Karnik S;  
 PI  
 XX WPI; 2003-833516/77.  
 DR  
 XX Use of an agent that promotes elastin signaling in smooth muscle cells  
 PT for e.g. decreasing or preventing occlusion of a body vessel by smooth  
 PT muscle cells, treating or preventing obstructive vascular disease, or  
 PT preventing stenosis.  
 PT  
 XX Claim 24; Page 138-141; Opp; English.  
 PS  
 XX The present invention relates to the use of an agent that promotes  
 CC elastin signaling in smooth muscle cells for decreasing or preventing  
 CC occlusion of a body vessel by smooth muscle cells, decreasing vascular  
 CC obstruction, promoting actin stress fiber formation or actin  
 CC polymerisation, increasing F:G actin ratio in a smooth muscle cell,  
 CC treating or preventing obstructive vascular disease (e.g. restenosis), or  
 CC preventing stenosis. The agent that promotes elastin signaling in smooth  
 CC muscle cells is useful for decreasing or preventing occlusion of a body

CC vessel by smooth muscle cells, decreasing vascular obstruction, promoting  
 CC actin stress fiber formation or actin polymerization, increasing F- $\alpha$   
 CC actin ratio in a smooth muscle cell, treating or preventing obstructive  
 CC vascular disease (e.g. restenosis following angioplasty), or preventing  
 CC stenosis. It is also useful in manufacturing a medicament for the  
 CC treatment or prevention of occlusion of a vessel. The present sequence is  
 CC the human tropoelastin protein as shown in the exemplification of the  
 CC invention

XX SQ Sequence 757 AA;

Query Match 100.0%; Score 59; DB 7; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 0.099;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALAAKAAKYGAA 13  
 |||||  
 Db 619 ALAAKAAKYGAA 631

RESULT 25  
 ADP65160  
 ID ADP65160 standard; protein; 757 AA.

XX AC ADP65160;

XX 12-AUG-2004 (first entry)

XX Human elastin.

XX autoimmune disease; arthritis; gene expression analysis;  
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;  
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;  
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;  
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
 KW immune; human.

XX Homo sapiens.

XX WO2003072827-A1.

PD 04-SEP-2003.

PF 31-OCT-2002; 2002WO-US035433.

XX 31-OCT-2001; 2001US-0336220P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Hirsch R, Thorton SL;

XX WPI; 2003-712740/67.  
 DR GENBANK; NP\_000492.

PT Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 PT gout.

XX Disclosure; Page; 56pp; English.

CC The invention relates to a novel method for diagnosing and analysing  
 CC autoimmune disease or arthritis. The method comprises obtaining a  
 CC patient sample containing mRNA, analysing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritis in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises: a treatment of rheumatoid arthritis; identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the

CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritis, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This sequence represents a  
 CC protein sequence relating to the genes used in the analysis and treatment  
 CC of autoimmune diseases or arthritis. Note: This sequence is not shown  
 CC in the specification. It has been supplied in an electronic format from  
 CC WIFO.

XX SQ Sequence 757 AA;

Query Match 100.0%; Score 59; DB 7; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 0.099;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALAAKAAKYGAA 13  
 |||||  
 Db 619 ALAAKAAKYGAA 631

RESULT 26

ADP40132  
 ID ADE40132 standard; protein; 711 AA.

XX AC ADE40132;

XX 29-JAN-2004 (first entry)

XX Human NOV16a protein - SEQ ID 38.

XX NOVX; cardiac; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
 KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
 KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;  
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
 KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
 KW tissue typing; human; NOV.

XX Homo sapiens.

XX WO2003064589-A2.

XX 07-AUG-2003.

XX 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

XX 03-AUG-2001; 2001US-0310291P.

XX 07-AUG-2001; 2001US-0310544P.

XX 08-AUG-2001; 2001US-0310951P.

XX 09-AUG-2001; 2001US-0311292P.

XX 13-AUG-2001; 2001US-0311979P.

XX 16-AUG-2001; 2001US-0312892P.

XX 17-AUG-2001; 2001US-0313201P.

XX 17-AUG-2001; 2001US-0313415P.

XX 20-AUG-2001; 2001US-0313643P.

XX 20-AUG-2001; 2001US-0313702P.

XX 21-AUG-2001; 2001US-0314031P.

XX 23-AUG-2001; 2001US-0314466P.

XX 28-AUG-2001; 2001US-0315403P.

XX 29-AUG-2001; 2001US-0315853P.

XX 17-SEP-2001; 2001US-0322716P.

XX 21-SEP-2001; 2001US-0323994P.

XX 14-DEC-2001; 2001US-0340233P.

XX 05-FEB-2002; 2002US-0354591P.

XX 19-MAR-2002; 2002US-0365478P.

XX 19-APR-2002; 2002US-0373814P.





XX WPI; 1999-132162/11.  
 DR N-PSDB; AAX27705.  
 XX  
 PT New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.  
 XX  
 PS Claim 7; Fig 3; 82pp; English.  
 XX  
 CC The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG)) binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents a human  
 CC tropoelastin derivative SHELDeltamodified  
 XX  
 SQ Sequence 660 AA;  
 Query Match 93.2%; Score 55; DB 2; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 0.43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALAAAKAAKYGA 12  
 Db 523 ALAAAKAAKYGA 534  
 RESULT 29  
 AAY69135  
 ID AAY69135 standard; protein; 515 AA.  
 AC AAY69135;  
 XX  
 DT 30-MAY-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human tropoelastin derivative.  
 XX  
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200004043-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 19-JUL-1999; 99WO-AU0000580.  
 XX  
 PR 17-JUL-1998; 98AU-00004723.  
 XX  
 PA (UNSY ) UNIV SYDNEY.  
 XX  
 PI Weiss AS;  
 XX  
 DR WPI; 2000-182399/16.  
 XX  
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.  
 XX  
 PS Disclosure; Page 131-133; 136pp; English.  
 XX  
 CC The present sequence represents a human tropoelastin derivative, which is  
 CC representative of tropoelastin derivatives of the invention. In the  
 CC tropoelastin derivatives of the invention a subsequence has been mutated  
 CC so that susceptibility to proteolysis is reduced or eliminated, or a  
 CC subsequence has been inserted so that susceptibility to proteolysis is  
 CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary

CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary  
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
 CC and for inducing chemotaxis. They are also useful for proliferation or  
 CC growth inhibition, particularly of smooth muscle cells, epithelial or  
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
 CC derivatives are competitive inhibitors of the protease, and are used for  
 CC protecting against lung damage caused by elastin, for inhibiting or  
 CC controlling localized growth of cancers or metastases, or to limit  
 CC protease activity that causes blood clotting  
 XX  
 SQ Sequence 515 AA;  
 Query Match 91.5%; Score 54; DB 3; Length 515;  
 Best Local Similarity 92.3%; Pred. No. 0.49;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ALAAAKAAKYGA 13  
 Db 281 ALAAAKAAKYGA 293  
 RESULT 30  
 AAY69071  
 ID AAY69071 standard; protein; 571 AA.  
 XX  
 AC AAY69071;  
 XX  
 DT 30-MAY-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human tropoelastin derivative.  
 XX  
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200004043-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 19-JUL-1999; 99WO-AU0000580.  
 XX  
 PR 17-JUL-1998; 98AU-00004723.  
 XX  
 PA (UNSY ) UNIV SYDNEY.  
 XX  
 PI Weiss AS;  
 XX  
 DR WPI; 2000-182399/16.  
 XX  
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.  
 XX  
 PS Disclosure; Page 115-117; 136pp; English.  
 XX  
 CC The present sequence represents a human tropoelastin derivative, which is  
 CC representative of tropoelastin derivatives of the invention. In the  
 CC tropoelastin derivatives of the invention a subsequence has been mutated  
 CC so that susceptibility to proteolysis is reduced or eliminated, or a  
 CC subsequence has been inserted so that susceptibility to proteolysis is  
 CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary

CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
CC and for inducing chemotaxis. They are also useful for proliferation or  
CC growth inhibition, particularly of smooth muscle cells, epithelial or  
CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
CC derivatives are competitive inhibitors of the protease, and are used for  
CC protecting against lung damage caused by elastin, for inhibiting or  
CC controlling localized growth of cancers or metastases, or to limit  
CC protease activity that causes blood clotting

XX Sequence 571 AA;

SQ Query Match 91.5%; Score 54; DB 3; Length 571;  
Best Local Similarity 92.3%; Pred. No. 0.55;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAAKAKYGAA 13  
| | | | | | | | | |  
Db 281 ALAAAKAKYGAA 293

Search completed: November 19, 2004, 16:28:39  
Job time : 6.65677 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 142.648 Seconds  
(without alignments)  
1755.321 Million cell updates/sec

Title: US-09-743-818A-5

Perfect score: 3615

Sequence: 1 GGVPGAIPGGVPGVFPYGA.....LSPIFGGACLGKACGRKRK 698

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A\_Geneseq\_23Sep04:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB ID	Description
1	3615	100.0	698	2	AAV01302	Human tro
2	3615	100.0	698	3	AAV69069	Amino aci
3	3602	99.6	730	5	AAO17360	Human ela
4	3602	99.6	730	8	ADQ19747	Human sof
5	3588.5	99.3	731	3	AAV69068	Human sof
6	3588.5	99.3	731	4	AAV66657	Human aci
7	3588.5	99.3	733	2	AAV56653	Human ela
8	3588.5	99.3	733	2	AAV01301	Synthetic
9	3588.5	99.3	757	7	ABG75223	Amino aci
10	3588.5	99.3	757	7	ADP65160	Human tro
11	3580.5	99.0	731	7	ADL96420	Human ela
12	3578.5	99.0	731	6	ABU08725	Human ela
13	3572	98.8	730	2	AAW46315	Human ela
14	3486.5	96.4	711	7	AAW08630	Human NOV
15	3485	96.4	712	3	AAW08631	Amino aci
16	3485	96.4	730	3	AAW08631	Fusion pr
17	3366	93.1	692	7	ADP40134	Human tro
18	3248.5	89.9	660	2	AAV01303	Human tro
19	3233.5	89.4	663	7	ADM03792	Human tro
20	3038	84.0	870	7	ADP08527	Human pro
21	2951.5	81.6	617	7	ADP64761	Human pro
22	2869	79.4	571	3	AAV69071	Amino aci
23	2680	74.1	515	3	AAV69135	Amino aci
24	2315.5	64.1	864	7	ADE56670	Rat Prote
25	1679	46.4	472	4	AAW88422	Human mem

26	1155	32.0	988	2	AAW80253	Polymer S
27	1155	32.0	988	5	ABP53474	Protein p
28	1150.5	31.8	832	2	AAW80252	Polymer S
29	1150.5	31.8	832	5	ABP53473	Protein p
30	1139.5	31.5	936	2	AAW80251	Polymer S
31	1139.5	31.5	936	5	ABP53472	Protein p
32	1133	31.3	745	2	AAV31682	Alanine-C
33	1131.5	31.3	1002	2	AAW09218	SELPOK po
34	1131.5	31.3	1002	2	AAW53544	Amino aci
35	1131.5	31.3	1002	3	AAV51888	Plasmid p
36	1131.5	31.3	1002	5	ABG31418	SELPOK pr
37	1131.5	31.3	1002	7	ABW01634	Plasmid p
38	1129.5	31.2	1412	2	AAW53519	Amino aci
39	1129.5	31.2	1413	1	AAW82957	ESBI prot
40	1129.5	31.2	1413	2	AAW41008	ESBI mult
41	1129.5	31.2	1413	2	AAW26343	ESBI synt
42	1129.5	31.2	1464	3	AAV78278	ESBI prot
43	1129.5	31.2	1465	5	ABG69268	Elastin-l
44	1129.5	31.2	1465	7	ADE44969	Recombina
45	1127	31.2	768	2	ABP53466	SELPO8 rel
46	1127	31.2	877	2	AAW80335	Protein p
47	1127	31.2	877	2	AAW49724	Protein p
48	1125.5	31.1	884	2	AAW80341	Protein p
49	1125.5	31.1	884	2	AAW09213	SELPO8 po
50	1125.5	31.1	884	2	AAW53541	Expected
51	1125.5	31.1	884	2	AAW49728	SELPO8 po
52	1125.5	31.1	884	3	AAV51882	Plasmid p
53	1125.5	31.1	884	5	ABG31412	SELPO8 po
54	1125.5	31.1	884	7	ABW01628	Plasmid p
55	1122.5	31.1	1056	2	AAW80254	Polymer S
56	1122.5	31.1	1056	5	ABP53475	Protein p
57	1115.5	30.9	768	5	ABP53481	Protein p
58	1109.5	30.7	972	2	AAW80255	Polymer S
59	1109.5	30.7	972	5	ABP53476	Protein p
60	1108.5	30.7	968	5	AAE18320	Silk elas
61	1108.5	30.7	2257	1	AAW82961	SELPL3 pro
62	1108.5	30.7	2257	2	AAW41012	SELPL3 mul
63	1108.5	30.7	2257	2	AAW26347	SELPL3 syn
64	1108.5	30.7	2257	2	AAW53523	Amino aci
65	1108.5	30.7	2257	3	AAV78282	SELPL3 ami
66	1108.5	30.7	2257	5	ABG69272	Silk/Elas
67	1108.5	30.7	2257	7	ADE44977	Recombina
68	1093.5	30.2	936	2	AAW09221	SELPOK-CS
69	1093.5	30.2	936	3	AAV51891	Plasmid p
70	1093.5	30.2	936	5	ABG31421	SELPOK-CS
71	1093.5	30.2	936	7	ABW01637	Plasmid p
72	1093.5	30.2	937	2	AAW53547	Amino aci
73	1092	30.2	1040	5	ABP53478	Protein p
74	1091.5	30.2	696	5	ABP53470	SELPOK re
75	1091.5	30.2	696	5	ABP53482	Protein p
76	1091.5	30.2	696	8	ADK51955	Repeat pr
77	1082	29.9	768	5	ABP53461	SELPL5 rel
78	1080	29.9	696	8	ADK51953	Repeat pr
79	1080	29.9	1024	2	AAW80256	Polymer S
80	1080	29.9	1024	5	ABP53477	Protein p
81	1074	29.7	2055	1	AAW82960	SELPL2 pro
82	1074	29.7	2055	2	AAW41011	SELPL2 mul
83	1074	29.7	2055	2	AAW26346	SELPL2 syn
84	1074	29.7	2055	2	AAW53522	Amino aci
85	1074	29.7	2055	3	AAV78281	SELPL2 ami
86	1074	29.7	2055	5	ABG69271	Silk/Elas
87	1074	29.7	2055	7	ADE44976	Recombina
88	1048.5	29.0	966	2	AAW09223	SELPOK-CS
89	1048.5	29.0	966	3	AAV51893	Plasmid p
90	1048.5	29.0	966	5	ABG31423	SELPOK-CS
91	1048.5	29.0	966	7	ABW01639	Plasmid p
92	1021	28.2	780	8	ADK51951	Repeat pr
93	1009.5	27.9	782	2	AAV31680	Fibronect
94	1009.5	27.9	782	2	AAV31695	Lysine-co
95	1006.5	27.8	1085	5	ABB05207	Elastin m
96	1004.5	27.8	979	1	AAW82958	ELPI prot
97	990	27.4	859	1	AAW82958	ELPI mul
98	990	27.4	859	2	AAW41009	ELPI mul

99 990 27.4 859 2 AAW26344 ELPI synt  
100 990 27.4 859 2 AAW53520 Amino aci

ALIGNMENTS

```
RESULT 1
ID AAY01302 standard; protein; 698 AA.
AC AAY01302;
XX 07-JUN-1999 (first entry)
XX Human tropoelastin variant SHELDelta26A.
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX Homo sapiens.
OS Synthetic.
XX WO9903886-A1.
XX 28-JAN-1999.
XX 17-JUL-1998; 98WO-AU000564.
XX 18-JUL-1997; 97AU-00008117.
XX (UNSY ) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 1999-132162/11.
XX New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
XX Claim 13; Fig 2; 82pp; English.
XX The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents the synthetic
CC human tropoelastin variant SHELDelta26A
XX
XX SQ Sequence 698 AA;
Query Match 100.0%; Score 3615; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 6.8e-202;
Matches 698; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGVPGAIPGGVPGGVYPGAGLGGALGGALGGKPLKVPVGGLAGNGLGAGLGAPPAVT 60
DB 1 GGVPGAIPGGVPGGVYPGAGLGGALGGALGGKPLKVPVGGLAGNGLGAGLGAPPAVT 60
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGVVPQPGAGVKGKVPGVGL 120
DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGVVPQPGAGVKGKVPGVGL 120
QY 121 PGVYPGGLVFGARFPGGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPPGPGQVPLGY 180
DB 121 PGVYPGGLVFGARFPGGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPPGPGQVPLGY 180
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QY 181 PIKAPKLPGGYGLPYTTTKLPGYGVGPGVAGAAKAGYPTGTGVGPQAAAAAATAAKAF 240
DB 181 PIKAPKLPGGYGLPYTTTKLPGYGVGPGVAGAAKAGYPTGTGVGPQAAAAAATAAKAF 240
QY 241 GAGAAAGVLPVGGAGVPGVPGAIPGIGIAGVGTAAAAAATAAKAGYGAAGLVPGG 300
DB 241 GAGAAAGVLPVGGAGVPGVPGAIPGIGIAGVGTAAAAAATAAKAGYGAAGLVPGG 300
QY 301 PGFPGVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVSPAAAAAATAAKAGYGAR 360
DB 301 PGFPGVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVSPAAAAAATAAKAGYGAR 360
QY 361 PGVGVGGIPTYGVGAGGPPGFGVGGIPGVAGVPSVGGVPGVPGVPGVISPAAAAA 420
DB 361 PGVGVGGIPTYGVGAGGPPGFGVGGIPGVAGVPSVGGVPGVPGVPGVISPAAAAA 420
QY 421 AKAAKYGVGTAAAAAATAAKAAQAQFGLVPGVGVAPGVAGVPGVPGVPGVAPG 480
DB 421 AKAAKYGVGTAAAAAATAAKAAQAQFGLVPGVGVAPGVAGVPGVPGVPGVAPG 480
QY 481 VGVAPGVVAPGIPGPGVAAAAAATAAKAAQAQFGLVPGVGVAGVPGVPGVPGV 540
DB 481 VGVAPGVVAPGIPGPGVAAAAAATAAKAAQAQFGLVPGVGVAGVPGVPGVPGV 540
QY 541 GVPGLGVGAGVPGVPGVAGVAAAAAATAAKAAQAQFGLVPGVGVAGVPGVPGV 600
DB 541 GVPGLGVGAGVPGVPGVAGVAAAAAATAAKAAQAQFGLVPGVGVAGVPGVPGV 600
QY 601 AAAAATAAKAAQAQFGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGVGGV 660
DB 601 AAAAATAAKAAQAQFGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGVGGV 660
QY 661 GGAGQFPLGGVAAAPGFGLSPIFGGACLGKACGKRK 698
DB 661 GGAGQFPLGGVAAAPGFGLSPIFGGACLGKACGKRK 698
```

```
RESULT 2
AAY69069
ID AAY69069 standard; protein; 698 AA.
XX
XX AC AAY69069;
XX 30-MAY-2000 (first entry)
DE Amino acid sequence of a human reduced tropoelastin derivative.
KW Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease;
KW antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;
KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
KW metastasis; blood clotting.
XX Synthetic.
OS Homo sapiens.
XX WO200004043-A1.
XX 27-JAN-2000.
XX 19-JUL-1999; 99WO-AU000580.
XX 17-JUL-1998; 98AU-00004723.
XX (UNSY ) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 2000-182399/16.
XX N-PSDB; AAZ61144.
XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
PT cell growth.
```

XX PS

Disclosure; Page 110-112; 136pp; English.

The present sequence represents a human reduced tropoelastin derivative, designated SHEL- $\alpha$ 26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting.

Sequence 698 AA;

Query Match 100.0%; Score 3615; DB 3; Length 698;  
Best Local Similarity 100.0%; Pred. No. 6.8e-202;  
Matches 698; Conservative 0; Mismatches 0; Indels 0

[illegible]

121 PGVPPGVLPQARPPGVVLPVPTGACVVKAPCVGAGAFAGIPGVPGPQPGVPLGY 180  
|  
147 PGVPPGVLPQARPPGVVLPVPTGACVVKAPCVGAGAFAGIPGVPGPQPGVPLGY 206  
|  
181 PIKAPKLPGGVGLPYTTTGLPKPYGPGGVAGAGAGYPTGTGVPQAAAAAATAAKAF 240  
|  
207 PIKAPKLPGGVGLPYTTTGLPKPYGPGGVAGAGAGYPTGTGVPQAAAAAATAAKAF 266  
|  
241 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAAKAAGVGLVPGG 300  
|  
267 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAAKAAGVGLVPGG 326  
|  
301 PGFPGVGVVPGAGVPGVPGVPGAGIPVPGAGIPGAAVPGVVSPEAAKAATAKYGAR 360  
|  
327 PGFPGVGVVPGAGVPGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAATAKYGAR 386  
|  
361 PGVGVGGIPTYGVGAGGFPFGVPGVGGIPGVAGVPSVGGVPGVPGVPGVSPQAQAAA 420  
|  
387 PGVGVGGIPTYGVGAGGFPFGVPGVGGIPGVAGVPSVGGVPGVPGVPGVSPQAQAAA 446  
|  
421 AKAAYGVGTAAAAAATAAKAQAQF-----GLVPGVGVAPGVGVAPGVGVGLAPG 474  
|  
447 AKAAYGVGTAAAAAATAAKAQAQFALLNLNLAGLVPGVGVAPGVGVGVGLAPG 506  
|  
475 VGVAPGVGVAPGVGVAPGVPGIPGGVAAAAAATAAKAQAQFALLNLNLAGLVPGVGV 534  
|  
507 VGVAPGVGVAPGVGVAPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 566  
|  
535 GLGVGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 594  
|  
567 GLGVGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 626  
|  
595 AGPAAAAAATAAKAQAQFGLVGAAGLVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 654  
|  
627 AGPAAAAAATAAKAQAQFGLVGAAGLVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 686  
|

RESULT 4

ADQ19747  
ID ADQ19747 standard; protein; 730 AA.  
AC ADQ19747;  
XX  
XX 26-AUG-2004 (first entry)  
XX  
XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.  
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.  
XX Homo sapiens.  
XX WO2004048938-A2.  
XX 10-JUN-2004.  
XX 26-NOV-2003; 2003WO-US038193.  
XX 26-NOV-2002; 2002US-0429739P.  
XX (PROT-) PROTEIN DESIGN LABS INC.  
XX Aziz N, Ginsburg WM, Zlotnik A;  
XX WPI; 2004-441208/41.  
XX

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue

PT sarcoma.

XX Example 2; SEQ ID NO 2566; 210pp; English.

PS The invention relates to a novel method for detecting soft tissue sarcoma  
XX which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytosolic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC protein of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 730 AA;

SQ Query Match 99.6%; Score 3602; DB 8; Length 730;  
Best Local Similarity 99.1%; Pred. No. 4e-201;  
Matches 698; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 GGVPGALIPGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 60  
Db 27 GGVPFALIPGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 86  
|  
Qy 61 PPGALVPGGVADAAAAAATAKAGAGLVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 120  
Db 87 PPGALVPGGVADAAAAAATAKAGAGLVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 146  
|  
Qy 121 PGVVPGGVLPQARPPGVVLPVPTGACVVKAPCVGAGAFAGIPGVPGPQPGVPLGY 180  
Db 147 PGVVPGGVLPQARPPGVVLPVPTGACVVKAPCVGAGAFAGIPGVPGPQPGVPLGY 206  
|  
Qy 181 PIKAPKLPGGVGLPYTTTGLPKPYGPGGVAGAGAGYPTGTGVPQAAAAAATAAKAF 240  
Db 207 PIKAPKLPGGVGLPYTTTGLPKPYGPGGVAGAGAGYPTGTGVPQAAAAAATAAKAF 266  
|  
Qy 241 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAAKAAGVGLVPGG 300  
Db 267 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAAKAAGVGLVPGG 326  
|  
Qy 301 PGFPGVGVVPGAGVPGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAATAKYGAR 360  
Db 327 PGFPGVGVVPGAGVPGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAATAKYGAR 386  
|  
Qy 361 PGVGVGGIPTYGVGAGGFPFGVPGVGGIPGVAGVPSVGGVPGVPGVPGVSPQAQAAA 420  
Db 387 PGVGVGGIPTYGVGAGGFPFGVPGVGGIPGVAGVPSVGGVPGVPGVPGVSPQAQAAA 446  
|  
Qy 421 AKAAYGVGTAAAAAATAAKAQAQF-----GLVPGVGVAPGVGVAPGVGVGLAPG 474  
Db 447 AKAAYGVGTAAAAAATAAKAQAQFALLNLNLAGLVPGVGVAPGVGVGVGLAPG 506  
|  
Qy 475 VGVAPGVGVAPGVGVAPGVPGIPGGVAAAAAATAAKAQAQFALLNLNLAGLVPGVGV 534  
Db 507 VGVAPGVGVAPGVGVAPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 566  
|  
Qy 535 GLGVGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 594  
Db 567 GLGVGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 626  
|  
Qy 595 AGPAAAAAATAAKAQAQFGLVGAAGLVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 654  
Db 627 AGPAAAAAATAAKAQAQFGLVGAAGLVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 686  
|  
Qy 655 GLGVVGGAGQFPFGVVAARPFGVLSPIPPGGACLGKACGRKK 698  
Db 687 GLGVVGGAGQFPFGVVAARPFGVLSPIPPGGACLGKACGRKK 730  
|



PI Rothstein A, Keeley F, Rothstein S, Stahl R;  
XX WPI; 2001-102886/11.  
XX Novel polypeptides that comprise three beta-sheet/beta-turn structures  
PT and are not naturally occurring fibrous protein, used to produce  
PT prosthesis suitable for implantation into humans, and cosmetic materials.  
XX  
XX Claim 1; Fig 1; 39pp; English.  
XX  
XX The present invention relates to a minimal functional unit (MFU) of human  
CC elastin polypeptide. This protein is useful in a cosmetic material or a  
CC prosthetic material such as prosthesis for blood vessel replacements, for  
CC heart valve replacement, tissue replacement, for covering burns, for  
CC covering wounds and stents  
XX  
XX Sequence 731 AA;  
SQ  
Query Match 99.3%; Score 3588.5; DB 4; Length 731;  
Best Local Similarity 95.5%; Pred. No. 2.4e-200;  
Matches 698; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
Qy 1 GGVPGAIPGGVPGGVYFPGAGLGGALGGKPLKPVPGGLAGAGLGAFFPAVT 60  
Db 1 GGVPGAIPGGVPGGVYFPGAGLGGALGGKPLKPVPGGLAGAGLGAFFPAVT 60  
Qy 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGVGAGAVVPPQAGVPGKVPVGL 120  
Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGVGAGAVVPPQAGVPGKVPVGL 120  
Qy 121 PGVTPGVLPGARFPGVGVLPQVPTGAGVKAPKAGVGGAFAGIPGVPGPQGVPLGY 180  
Db 121 PGVTPGVLPGARFPGVGVLPQVPTGAGVKAPKAGVGGAFAGIPGVPGPQGVPLGY 180  
Qy 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGVPQAAAAKAAKAF 240  
Db 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGVPQAAAAKAAKAF 240  
Qy 241 GAGAAGVLPVGGAGVPGVPGAIPGIGTAGVGTTPAAAAAATAKAAKAGLIVPGG 300  
Db 241 GAGAAGVLPVGGAGVPGVPGAIPGIGTAGVGTTPAAAAAATAKAAKAGLIVPGG 300  
Qy 301 PGFPGVGVPGAGVPGVPGAIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 360  
Db 301 PGFPGVGVPGAGVPGVPGAIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 360  
Qy 361 PGVGVGGIPTTYGVGAGGPGFPGVGVGIPGVAGVPSVGVPGVGVGIPSPQAQAAA 420  
Db 361 PGVGVGGIPTTYGVGAGGPGFPGVGVGIPGVAGVPSVGVPGVGVGIPSPQAQAAA 420  
Qy 421 AKAAKYGVGTTPAAAAAATAKAAKAGLIVPGVAGVPGVAGVPGVAGVPGVAGV 480  
Db 421 AKAAKYGVGTTPAAAAAATAKAAKAGLIVPGVAGVPGVAGVPGVAGVPGVAGV 480  
Qy 481 VGVAPGVAGVPGIPGGVAAAAKAAKAAQALRAAGLGAAGIPGLGVGVPGVGVGA 540  
Db 481 VGVAPGVAGVPGIPGGVAAAAKAAKAAQALRAAGLGAAGIPGLGVGVPGVGVGA 540  
Qy 541 GVPGLGVAGVPGFGA-----VPGALAAKAA 567  
Db 541 GVPGLGVAGVPGFAGAGDEGVRRSLSPELREGDPSSQHLPTSPSPRVPGALAAKAA 600  
Qy 569 KYGAAPVGLGLGALGVGIPGVVVGAGPAAAAAATAKAAKAAQGLVGAAGLGLGVG 627  
Db 601 KYGAAPVGLGLGALGVGIPGVVVGAGPAAAAAATAKAAKAAQGLVGAAGLGLGVG 660  
Qy 628 GLGVPGVGLGGLIPAAAAAATAKAAKAAAGLGVGAGQFPLGGVAAAPGFLSPIPGGA 687  
Db 661 GLGVPGVGLGGLIPAAAAAATAKAAKAAAGLGVGAGQFPLGGVAAAPGFLSPIPGGA 720  
Qy 688 CLGKACGRKK 698  
Db 721 CLGKACGRKK 731

RESULT 7  
AAR56653  
ID AAR56653 standard; protein; 733 AA.  
XX AAR56653;  
AC AAR56653;  
XX  
DT 25-MAR-2003 (revised)  
DT 22-MAR-1995 (first entry)  
XX  
DE Synthetic human tropoelastin (SHEL).  
XX  
KW Tropoelastin; pharmaceutical; surgical dressing.  
XX  
OS Synthetic.  
XX  
XX WO9414958-A1.  
XX  
XX 07-JUL-1994.  
XX  
XX 16-DEC-1993; 93WO-AU000655.  
XX  
XX 22-DEC-1992; 92AU-00006520.  
PR 28-JUN-1993; 93AU-00009661.  
XX  
XX (UNSY ) UNIV SYDNEY.  
XX  
XX Weiss AS, Martin SL;  
PI WPI; 1994-263633/32.  
DR N-PSDB; AAQ70941.  
XX  
XX Synthetic polynucleotide(s) - encode recombinant tropoelastins and  
PT variants.  
PS  
PS Disclosure; Page 30; 77pp; English.  
XX  
XX Human synthetic tropoelastin is susceptible to hydrolytic breakdown of  
CC the crosslinks. Such material may be useful in e.g. surgical  
CC applications, where the gradual loss of material over time is intended.  
CC (Updated on 25-MAR-2003 to correct FN field.)  
SQ  
Sequence 733 AA;  
Query Match 99.3%; Score 3588.5; DB 2; Length 733;  
Best Local Similarity 95.5%; Pred. No. 2.4e-200;  
Matches 698; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
Qy 1 GGVPGAIPGGVPGGVYFPGAGLGGALGGKPLKPVPGGLAGAGLGAFFPAVT 60  
Db 3 GGVPGAIPGGVPGGVYFPGAGLGGALGGKPLKPVPGGLAGAGLGAFFPAVT 62  
Qy 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGVGAGAVVPPQAGVPGKVPVGL 120  
Db 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGVGAGAVVPPQAGVPGKVPVGL 122  
Qy 121 PGVTPGVLPGARFPGVGVLPQVPTGAGVKAPKAGVGGAFAGIPGVPGPQGVPLGY 180  
Db 123 PGVTPGVLPGARFPGVGVLPQVPTGAGVKAPKAGVGGAFAGIPGVPGPQGVPLGY 182  
Qy 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGVPQAAAAAATAKAAKAF 240  
Db 183 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGVPQAAAAAATAKAAKAF 242  
Qy 241 GAGAAGVLPVGGAGVPGVPGAIPGIGTAGVGTTPAAAAAATAKAAKAGLIVPGG 300  
Db 243 GAGAAGVLPVGGAGVPGVPGAIPGIGTAGVGTTPAAAAAATAKAAKAGLIVPGG 302  
Qy 301 PGFPGVGVPGAGVPGVPGAIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 360  
Db 303 PGFPGVGVPGAGVPGVPGAIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 362









of lamprin comprising at least three beta sheets/beta turns, and (d) a polypeptide consisting essentially of a spider silk protein comprising at least three beta sheets/beta turns, a polypeptide having the primary structure of a portion of a naturally occurring fibrous protein and a secondary structure comprising at least three beta sheets/beta turns, where each of the beta sheet/beta turn structures comprises from 3 to about 7 amino acids and the polypeptide is not a naturally occurring fibrous protein. The minimal functional unit (MFU) of the invention is useful to construct human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing. Alternatively, the MFU can be co-aggregated with other proteins, for example collagen, to provide prosthetic material that resembles the natural structural materials of the body. The MFU based material is subject to infiltration of cells growing in the patient, including endothelial cells, and the prosthesis can become a permanent living tissue replacement. The material is more biocompatible than other elastin-containing materials proposed for prostheses.

Query Match	99.0%;	Score 3580.5;	DB 7;	Length 731;
Best Local Similarity	95.3%;	Pred. No. 7e-200;		
Matches 697;	Conservative 0;	Mismatches 1;	Indels 33;	Gaps 1;
Qy	1	GGVPGATPGGVGGVFFYPGAGLGGALGGALCPGGKPLKPVDPGGLAGAGLGGALGAFPAVT	60	
Db	1	GGVPGALPGGVGGVFFYPGAGLGGALGGALCPGGKPLKPVDPGGLAGAGLGGALGAFPAVT	60	
Qy	61	FPGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGGGLGVSAGAVVPQPGAGVPGKVPGVGL	120	
Db	61	FPGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGGGLGVSAGAVVPQPGAGVPGKVPGVGL	120	
Qy	121	PGVVPGGVLPGARPPGCVGLPCVPTGAGVKPKAPQVGGAFAGIPGVGPFPGQPQGVPLGY	180	
Db	121	PGVVPGGVLPGARPPGCVGLPCVPTGAGVKPKAPQVGGAFAGIPGVGPFPGQPQGVPLGY	180	
Qy	181	PIKAPKLPGGYGLPVTYTKGLPYGYPGGVAGAGKAGYPTCTGVGPQAAAAAAYKAAAKF	240	
Db	181	PIKAPKLPGGYGLPVTYTKGLPYGYPGGVAGAGKAGYPTCTGVGPQAAAAAAYKAAAKF	240	
Qy	241	GAGAAGVLPVGGAGVPGVPGAIPIGGIAGVGTPTAAAAAAYKAAKYGAAAGLVPGG	300	
Db	241	GAGAAGVLPVGGAGVPGVPGAIPIGGIAGVGTPTAAAAAAYKAAKYGAAAGLVPGG	300	
Qy	301	PGFPGVGVDPGAGVPGVGVDPGAGIPVTPGAGIPGAAVPGVVSPEAAAKAAKAAKYGAR	360	
Db	301	PGFPGVGVDPGAGVPGVGVDPGAGIPVTPGAGIPGAAVPGVVSPEAAAKAAKAAKYGAR	360	
Qy	361	PGVGVGGIPTVGVGAGGPPGCVGVGGIPGVAGVPSVGVPGVGGVPGVGVISPEAQAAAA	420	
Db	361	PGVGVGGIPTVGVGAGGPPGCVGVGGIPGVAGVPSVGVPGVGGVPGVGVISPEAQAAAA	420	
Qy	421	AKAAKYGVGTPAAAAAAYKAAKAAQFGLVPGVGAVPGVGVAPGVGVAPGVGVAPG	480	
Db	421	AKAAKYGVGTPAAAAAAYKAAKAAQFGLVPGVGAVPGVGVAPGVGVAPGVGVAPG	480	
Qy	481	VGVAPGVGAPGIPGGVYAAAKSAKVAAKAQLRAAAGLGGAGIPGLGVGVGVPGLGVGA	540	
Db	481	VGVAPGVGAPGIPGGVYAAAKSAKVAAKAQLRAAAGLGGAGIPGLGVGVGVPGLGVGA	540	
Qy	541	GVPLGVGAGVPGFGA-----VPGALAAKAA	567	
Db	541	GVPLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSQHLPTSPSSPRVPGALAAKAA	600	
Qy	568	KYGAAPGVGLGGIAGLGGVGIIPGVGVGAGPAAAAAAYKAAKAAQFGLVCAAGLGGLVG	627	
Db	601	KYGAAPGVGLGGIAGLGGVGIIPGVGVGAGPAAAAAAYKAAKAAQFGLVCAAGLGGLVG	660	
Qy	628	GLGVPGVGGIGGTPAAAAAAYKAAKYGAAGLGGVLGGAGQFPLGGVAARPQFGLSPIFP	697	
Db	661	GLGVPGVGGIGGTPAAAAAAYKAAKYGAAGLGGVLGGAGQFPLGGVAARPQFGLSPIFP	720	
Qy	688	CLGKACGRREK	698	

Db	721	CLGKACGRKRK	731
RESULT 12			
ABU08725			
ID	ABU08725	standard; protein; 731 AA.	
XX	AC		
XX	ABU08725;		
AC			
XX	25-JUN-2003	(first entry)	
DT			
XX	Human elastin	mature protein.	
DE			
XX	Human;	elastin; minimal functioning;	
KW	beta-sheet/beta-turn structure; fibrous		
KW	beta vessel replacement; heart replacement		
KW	spider silk; cord; rope; parachute		
KW	platelet activation inhibitor; non-		
KW	non-immunogenic; biocompatible; high		
KW	plasticity.		
XX			
XX	Homo sapiens.		
OS			
XX			
XX	US6489446-B1.		
PN			
XX			
XX	03-DEC-2002.		
PD			
XX			
XX	29-JUN-1999;	99US-00340736.	
PF			
XX			
XX	07-AUG-1996;	96US-0023522P.	
PR			
XX	07-AUG-1997;	97US-00911364.	
XX			
XX	(HSCR-) HSC RES & DEV LP.		
PA	(PROT-) PROTEIN SPECIALTIES LTD.		
XX			
PI	Rothstein A, Keeley F, Rothstein		
XX			
XX	WPI; 2003-391056/37.		
DR			
XX			
XX	Novel polypeptide useful in prostheses		
PT	characterized by three beta-sheets		
PT	naturally occurring fibrous proteins		
PT			
XX			
PS	Claim 1; Fig 1B; 21pp; English.		
XX			
CC	The invention describes a polypeptide		
CC	functioning unit (MFU) which is pro-		
CC	and comprised of at least three beta		
CC	at least one amino acid residue that		
CC	a naturally occurring fibrous protein		
CC	construct human elastin-like protein		
CC	replacement, heart replacement val-		
CC	burns or wounds to promote healing		
CC	proteins, for e.g. collagen, to pro-		
CC	resembles the natural structural m-		
CC	lamrin and other fibrous proteins		
CC	a variety of materials, for a number		
CC	in cords and ropes for use in para-		
CC	synthetic prosthesis with MFUs mod-		
CC	inhibits platelet binding and acti-		
CC	more biocompatible than other elasti-		
CC	to solubilised fragments of elastin		
CC	peptide of defined composition. The		
CC	parent protein, simpler in structure		
CC	quantity, to handle in solution an		
CC	practical purposes. Like other elasti-		
CC	thrombogenic and provides a friend-		
CC	being composed entirely of a human		
CC	immunogenic, thus providing a truly		
CC	on lamrin and other fibrous protein		
CC	materials having high tensile stre-		
CC	their parent proteins. This is the		
CC			

Novel polypeptide useful in prosthesis, has a secondary structure characterized by three beta-sheet/beta-turn structures, and is not a naturally occurring fibrous protein.

WPI: 2003-391056/37.

WPI: 2003-391056/37.

...metastatic disease is not a secondary structure

characterized by three beta-sheet/beta-naturally occurring fibrous protein.

# Cum gratia

The invention describes a polypeptide (I) comprising a minimal functioning unit (MFU) which is present in the sequence of human elastin and comprised of at least three beta-sheet/beta-turn structures, and at least one amino acid residue that participates in cross-linking, and not a naturally occurring fibrous protein. The MFU material can be used to construct human elastin-like prostheses such as tubes for blood vessel replacement, heart replacement valves and sheets for other uses such as burns or wounds to promote healing. MFUs can be co-aggregated with other proteins, for e.g. collagen, to provide prosthesis material that resembles the natural structural materials of the body. MFUs modeled on laminin and other fibrous proteins e.g. spider silk, can be used to make a variety of materials, for a number of different applications, for e.g. in cords and ropes for use in parachutes and in cosmetics. Coating synthetic prostheses with MFUs modeled on human elastin significantly inhibits platelet binding and activation. The human-like MFU material is more biocompatible than other elastin-containing materials. In contrast to solubilised fragments of elastin used before, an MFU is a single peptide of defined composition. The MFU is considerably smaller than the parent protein, simpler in structure, easier to produce or express in quantity, to handle in solution and to manipulate for experimental and practical purposes. Like other elastin preparations, the MFU is non-thrombogenic and provides a friendly environment for cell infiltration. Being composed entirely of a human elastin sequence, MFU is non-immunogenic, thus providing a truly biocompatible material. MFUs modeled on laminin and other fibrous proteins can be used to make a variety of materials having high tensile strength, elasticity and plasticity of their parent proteins. This is the amino acid sequence of mature human

CC elastin on which the MFU peptides of the invention are based

XX Sequence 731 AA;

Query Match 99.0%; Score 3578.5; DB 6; Length 731;  
Best Local Similarity 95.2%; Pred. No. 9.2e-200;  
Matches 696; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

```
QY 1 GGVPCALPGGVPGGVFFPGAGLGGALGGKPLKPVPGGLAGAGLGAFAFPAVT 60
DB 1 GGVPCALPGGVPGGVFFPGAGLGGALGGKPLKPVPGGLAGAGLGAFAFPAVT 60
QY 61 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGLVSGAVVPPQPGKVPKPVGVL 120
DB 61 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGLVSGAVVPPQPGKVPKPVGVL 120
QY 121 PGVYVPGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAFAGIPGVGPQGPVPLGY 180
DB 121 PGVYVPGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAFAGIPGVGPQGPVPLGY 180
QY 181 PIKAPKLPGGYGLPYTTGKLPYGGPGGVAGAAKAGYPTGTGVPQAAAAAATAAKAF 240
DB 181 PIKAPKLPGGYGLPYTTGKLPYGGPGGVAGAAKAGYPTGTGVPQAAAAAATAAKAF 240
QY 241 GAGAAGVLPVGGAGVPGVPGALIPGIGGIAGVGTAAAAAATAAKAGYGAAGLVPFG 300
DB 241 GAGAAGVLPVGGAGVPGVPGALIPGIGGIAGVGTAAAAAATAAKAGYGAAGLVPFG 300
QY 301 PFGPGVGVGVPAGVPGVPGAGIPVVPAGIPGAAPVPGVSPVPEAAAAAATAAKYGAR 360
DB 301 PFGPGVGVGVPAGVPGVPGAGIPVVPAGIPGAAPVPGVSPVPEAAAAAATAAKYGAR 360
QY 361 PGVGVGGIPTYGVGAGGFFPGFVGVGIPGVAGVPSVGGVPGVPGVGGISPEAAAAA 420
DB 361 PGVGVGGIPTYGVGAGGFFPGFVGVGIPGVAGVPSVGGVPGVPGVGGISPEAAAAA 420
QY 421 AKAAKYGVGTAAAAAATAAKAAQFGLVPGVAPGVGVPAGVAPGVGLAPGVGVPAG 480
DB 421 AKAAKYGVGTAAAAAATAAKAAQFGLVPGVAPGVGVPAGVAPGVGLAPGVGVPAG 480
QY 481 VGVAPGVGVPAGIPGCGVAAAAAATAAKAAQFGLVPGVAPGVGVPAGVAPGVGLAPGV 540
DB 481 VGVAPGVGVPAGIPGCGVAAAAAATAAKAAQFGLVPGVAPGVGVPAGVAPGVGLAPGV 540
QY 541 VPGVGLGVGAGVPGFGA-----VPGALAAAKAA 567
DB 541 VPGVGLGVGAGVPGFGADEGVRRSLSPELREGDPSSSOHLPTSPSPVPGALAAAKAA 600
QY 568 KYGAAVPGVGLGGLGALGGVIGIPGVVAGPAAAAAATAAKAAQFGLVGAAGLGLGVG 627
DB 601 KYGAAVPGVGLGGLGALGGVIGIPGVVAGPAAAAAATAAKAAQFGLVGAAGLGLGVG 660
QY 628 GLGVPGVGLGGIPPAATAAKAAKYGAAGLGGVGLGAGQFPLGVGAAPFGFLSPITPGA 687
DB 661 GLGVPGVGLGGIPPAATAAKAAKYGAAGLGGVGLGAGQFPLGVGAAPFGFLSPITPGA 720
QY 688 CLGKACGRKRK 698
DB 721 CLGKACGRKRK 731
```

RESULT 13

AAW46315

ID AAW46315 standard; protein; 730 AA.

XX

AC AAW46315;

XX

DT 23-JUL-1998 (first entry)

XX

DE Human elastin containing non-natural polypeptide MFU-1 sequence.

XX

KW MFU-1; minimal functional unit; elastin; human; fibrous protein;

KW beta-sheet; coating; wound dressing.

XX Homo sapiens.

XX Key Location/Qualifiers  
XX Protein 374..499  
XX /note= "MFU-1 polypeptide"

XX WO9805685-A2.

XX 12-FEB-1998.

XX 07-AUG-1997; 97WO-CA000560.

XX 07-AUG-1996; 96US-0023552P.

XX 07-AUG-1997; 97US-00911364.

XX (PROT-) PROTEIN SPECIALTIES LTD.

XX (HOSP-) HOSPITAL FOR SICK CHILDREN.

XX Rothstein A, Keeley FW, Rothstein SJ;

XX MPI; 1998-145551/13.

XX New non-natural polypeptide with multiple beta-sheet, beta-turn structures - particularly based on human elastin, useful for coating prostheses, as wound dressings, etc., allows ingrowth of cells.

XX Claim 5; Fig 1B; 39pp; English.

XX This represents the human elastin sequence containing the minimal functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a polypeptide that has at least 3 beta-sheet/beta-turn structures, but is not a naturally occurring fibrous protein. Each beta-sheet structure has 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at least 1 amino acid that can take part in crosslinking. The polypeptide can also be derived from the sequences of animal elastin, lamprlin and spider silk protein. The MFU polypeptides are self-aligning peptides having the same primary structure as part of a natural fibrous protein. They are used to coat prostheses made of animal or synthetic material or metal, particularly for use as blood vessel or heart valve replacements, wound or burn dressings, or stents. They can be used in cosmetic, elastic or high-tensile strength materials, e.g. ropes or parachute cords. Prostheses based on the MFU allow penetration of endothelial cells, so become permanent, living, tissue replacements. The MFU polypeptides have better biocompatibility than known elastin-based materials. They are well defined, homogeneous material and are easier to manipulate and produce than full-length elastins. They are non-thrombogenic and non-immunogenic. Materials can be made from 2 or more different MFU polypeptides to allow properties to be tailored for particular applications, e.g. combining the high extensibility of elastin and the high tensile strength of spider silk protein

XX Sequence 730 AA;

QY Query Match

Best Local Similarity 98.8%; Score 3572; DB 2; Length 730;

Matches 697; Conservative 0; Mismatches 0; Indels 34; Gaps 2;

QY 1 GGVPCALPGGVPGGVFFPGAGLGGALGGKPLKPVPGGLAGAGLGAFAFPAVT 60

DB 1 GGVPCALPGGVPGGVFFPGAGLGGALGGKPLKPVPGGLAGAGLGAFAFPAVT 60

QY 61 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGLVSGAVVPPQPGKVPKPVGVL 120

DB 61 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGLVSGAVVPPQPGKVPKPVGVL 120

QY 121 PGVYVPGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAFAGIPGVGPQGPVPLGY 180

DB 121 PGVYVPGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAFAGIPGVGPQGPVPLGY 180

QY 181 PIKAPKLPGGYGLPYTTGKLPYGGPGGVAGAAKAGYPTGTGVPQAAAAAATAAKAF 240

DB 181 PIKAPKLPGGYGLPYTTGKLPYGGPGGVAGAAKAGYPTGTGVPQAAAAAATAAKAF 240

PR	20-AUG-2001; 2001US-0313643P.
PR	20-AUG-2001; 2001US-0317022P.
PR	21-AUG-2001; 2001US-0314031P.
PR	23-AUG-2001; 2001US-0314466P.
PR	28-AUG-2001; 2001US-0315403P.
PR	29-AUG-2001; 2001US-0315853P.
PR	17-SEP-2001; 2001US-0322716P.
PR	21-SEP-2001; 2001US-0323994P.
PR	14-DEC-2001; 2001US-0340233P.
PR	05-FEB-2002; 2002US-0354591P.
PR	19-MAR-2002; 2002US-0365478P.
PR	19-APR-2002; 2002US-0373814P.
PR	19-APR-2002; 2002US-0373825P.
PR	19-APR-2002; 2002US-0373989P.
PR	23-APR-2002; 2002US-0374632P.
PR	07-JUN-2002; 2002US-0386971P.
PR	01-AUG-2002; 2002US-0021017Z.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
PI	Shinkets RA, Zernhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
PI	Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
PI	Guo X, Zhong M, Gerlach VL, Hjalte T, Rastelli L, Spytek KA;
PI	Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
PI	Alsbrook JP, Lepley DM, Burgess CB, Majumder K, Wolenc AR;
PI	Smithson G;
XX	
DR	WPI; 2003-663472/62.
DR	N-PSDB; ADE40131.
XX	
PT	New NOVX polypeptides and nucleic acids, useful for preventing or
PT	treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT	atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT	pharmacogenomics.
XX	
PS	Claim 1; SEQ ID NO 38; 560pp; English.
XX	
CC	The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC	invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
CC	cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC	neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
CC	gynaecological activities and may be useful in diagnosing, treating or
CC	preventing NOVX-associated disorders including cardiomyopathy,
CC	atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
CC	sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC	disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC	be utilised as vaccines whilst the nucleic acids may be used as
CC	hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC	preventive medicine and pharmacogenomics. The current sequence is that of
CC	the human NOV protein of the invention.
XX	
SQ	Sequence 711 AA;
	Query Match 96.4%; Score 3486.5; DB 7; Length 711;
	Best Local Similarity 96.6%; Pred. No. 1.9e-194;
	Matches 679; Conservative 1; Mismatches 0; Indels 23; Gaps 2
QY	1 GGVPGAIPGGVPGGVFPYGAGLGGGALGCGKPLKVPVGGLAGAGLGAFPAYT 60
Db	27 GGVPGAIPGGVPGGVFPYGAGLGGGALGCGKPLKVPVGGLAGAGLGAFPAYT 86
QY	61 FPGALVPGGVADAAAAYKAAGAGLGGVPGVGLGVS-----GAUVPPGAGVKPFKV 115
Db	87 FPGALVPGGVADAAAAYKAAGAGLGGVPGVGLGVSAAAPSVPGANVFPNGNVFPGKV 146
QY	116 PGVGLPGVPGGVLPGARFPVGVLPGVPTGACVKFKAPCVGGAFAFIPGVFGFPQG 175
Db	147 PGVGLPGVPGGVLPGARFPVGVLPGVPTGACVKFKAPCVGGAFAFIPGVFGFPQG 206
QY	176 VPLGYTPKAPKLPGGGLPYTTOKLPYGVPGGVAGAAGKAGVPTGTGVCQPAAAAAK 235
Db	207 VPLGYTPKAPKLPGGGLPYTTOKLPYGVPGGVAGAAGKAGVPTGTGVCQPAAAAAK 266









PR 28-AUG-2001; 2001US-0315403P.  
PR 29-AUG-2001; 2001US-0315853P.  
PR 17-SEP-2001; 2001US-0322716P.  
PR 21-SEP-2001; 2001US-0323994P.  
PR 14-DEC-2001; 2001US-0340233P.  
PR 05-FEB-2002; 2002US-0354591P.  
PR 19-MAR-2002; 2002US-0365478P.  
PR 19-APR-2002; 2002US-0373814P.  
PR 19-APR-2002; 2002US-0373825P.  
PR 19-APR-2002; 2002US-0373989P.  
PR 23-APR-2002; 2002US-0374632P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 01-AUG-2002; 2002US-00210172.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;  
PI Shimkets RA, Zerhusen BD, Li L, Padigaru M, Casman SJ;  
PI Voess EZ, Boidog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;  
PI Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytke KA;  
PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;  
PI Alsbrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;  
PI Smithson G;  
XX  
DR WPI: 2003-663472/62.  
DR N-PSDB; ADE40133.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
PS Claim 1; SEQ ID NO 40; 560pp; English.  
XX  
CC The invention relates to a novel NOVX polypeptide. The polypeptide of the  
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,  
CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and  
CC synaecological activities and may be useful in diagnosing, treating or  
CC preventing NOVX-associated disorders including cardiomyopathy,  
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple  
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
CC be utilised as vaccines whilst the nucleic acids may be used as  
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
CC preventive medicine and pharmacogenomics. The current sequence is that of  
CC the human NOV protein of the invention.  
XX  
SQ Sequence 692 AA;

Query Match 93.1%; Score 3366; DB 7; Length 692;  
Best Local Similarity 93.8%; Pred. No. 1.8e-187;  
Matches 660; Conservative 0; Mismatches 0; Indels 44; Gaps 2;

QY 1 GGVPGNIPGVGGVYFPGAGLGGALGPGKPLKVPVPGLAGAGLGAGFPAPT 60  
Db |||||  
QY 27 GGVPGNIPGVGGVYFPGAGLGGALGPGKPLKVPVPGLAGAGLGAGFPAPT 86  
Db |||||  
QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVGGVGGVGGVGGVGGVGGVGGV 120  
Db |||||  
QY 87 FPGALVPGGVADAAAYKAAKAGAGLGGVGGVGGVGGVGGVGGVGGVGGV 141  
Db |||||  
QY 121 PGVYGGVLPGARFPGVGVLPVPTGAGVKPKAPGVGAFAGIPGVPGPQGVPLGY 180  
Db |||||  
QY 142 -----PGVGGAFAGIPGVPGPQGVPLGY 168  
Db |||||  
QY 181 PIKAPLPGVGLPVTTKLPYGVPGGVAGAGKAGYPTGTGVGFQAAAAAKAAKF 240  
Db |||||  
QY 169 PIKAPLPGVGLPVTTKLPYGVPGGVAGAGKAGYPTGTGVGFQAAAAAKAAKF 228  
QY 241 GAGAGVLPVGGVGGVPGVGNIPGIGTGTGTPAAAAAKAAKAYGAAAGLVPGG 300  
Db |||||  
QY 229 GAGAGVLPVGGVGGVPGVGNIPGIGTGTGTPAAAAAKAAKAYGAAAGLVPGG 288  
Db |||||

QY 301 PGFPGVGVPGAGVPGVGVPGAGIPVVPAGIPGAAVPGVVSPEAAAKAAKAYGAR 360  
Db |||||  
QY 289 PGFPGVGVPGAGVPGVGVPGAGIPVVPAGIPGAAVPGVVSPEAAAKAAKAYGAR 348  
Db |||||  
QY 361 PGVGGGIPVTVGGAGGPGFPGVGGIPGVAGVPSVGGVPGVGVGGVGGVGGV 420  
Db |||||  
QY 349 PGVGGGIPVTVGGAGGPGFPGVGGIPGVAGVPSVGGVPGVGVGGVGGVGGV 408  
Db |||||  
QY 421 AKAAKYGVGTAAAAAKAAKAAAF-----GLVPGVGVAPGVGVAGVPGVGLAPG 474  
Db |||||  
QY 409 AKAAKYGVGTAAAAAKAAKAAAFALLNLNLAGLVFGVGVAPGVGVAGVGLAPG 468  
Db |||||  
QY 475 VGVAPGVGVAPGVGVAPGVGGVGGVAAAKAAKAAQAAAAAGLGGAGIPGLGVGVGP 534  
Db |||||  
QY 469 VGVAPGVGVAPGVGVAPGVGGVGGVAAAKAAKAAQAAAAAGLGGAGIPGLGVGVGP 528  
QY 535 GLGVGAGVPGVGLGVGAGVPGVGVAGVPGVLAALAAKAAKAAVPGVGLGALGVGPGV 594  
Db |||||  
QY 529 GLGVGAGVPGVGLGVGAGVPGVGVAGVPGVLAALAAKAAKAAVPGVGLGALGVGPGV 588  
QY 595 AGPAAAAAKAAKAAKAAQFGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGV 654  
Db |||||  
QY 589 AGPAAAAAKAAKAAKAAQFGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGV 648  
QY 655 GLGVGAGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 698  
Db |||||  
QY 649 GLGVGAGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 692  
Db |||||

RESULT 18  
AA001303  
ID AAY01303 standard; protein; 660 AA.  
XX  
AC AAY01303;  
XX  
DT 07-JUN-1999 (first entry)  
XX  
DE Human tropoelastin derivative SHELDELtAmoDified.  
XX  
KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmacological; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO9903886-A1.  
XX  
PD 28-JAN-1999.  
XX  
PF 17-JUL-1998; 98WO-AU000564.  
XX  
PR 18-JUL-1997; 97AU-00008117.  
XX  
PA (UNSY ) UNIV SYDNEY.  
XX  
PI Weiss AS;  
XX  
DR WPI: 1999-132162/11.  
DR N-PSDB; AAX27705.  
XX  
PT New derivatives of human tropoelastin - with elastin-like or  
PT macromolecular binding properties, useful e.g. as surgical implants.  
XX  
PS Claim 7; Fig 3; 82pp; English.  
XX  
CC The invention relates to a derivative or variant of human tropoelastin  
CC (hTE) having elastin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives  
CC or hybrid proteins containing the derivatives are useful in medical,

CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26A, from hIE. The present sequence represents a human  
CC tropoelastin derivative SHELDeltamodified  
XX  
SQ Sequence 660 AA;  
  
Query Match 89.9%; Score 3248.5; DB 2; Length 660;  
Best Local Similarity 91.7%; Pred. No. 1.1e-180;  
Matches 644; Conservative 3; Mismatches 8; Indels 47; Gaps 6;  
  
QY 1 GGVPCALPGGVPGGVFFYFAGLGGALGGGKPLKVPVGGLAGLGGAGLGAFAVPT 60  
Db 2 GGVPCALPGGVPGGVFFYFAGLGG----- 25  
  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVPQPGAGVKGVPVGL 120  
Db 26 -----VPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVPQPGAGVKGVPVGL 80  
  
QY 121 PGVYVPG--GVLPAGAFPGVGLPGVPTGAGVKKPKAPGVGGAFAGIPGVGPGQPGVPLG 179  
Db 81 PGVYVPGFCAVPGAFPGVGLPGVPTGAGVKKPKAPGVGGAFAGIPGVGPGQPGVPLG 140  
  
QY 180 YPIKAPKLPGGVGLPYTTTKLPGYGGVPGGVAAGAGKAGYPTGTGVPQAAAAAATAAK 239  
Db 141 YPIKAPKLPGGVGLPYTTTKLPGYGGVPGGVA--AAGKAGYPTGTGVPQAAAAAATAAK 199  
  
QY 240 FGAAGAA--GVLPVGGAGVPGVPAIPGTTGGTAGVTPAAAAAATAAKAAYGAAAGLV 297  
Db 200 FGAAGAGFAGVGGVGGVPGVPAIPGTTGGTAGVTPAAAAAATAAKAAYGAAAGLV 259  
  
QY 298 PGGPFGPGVGVPGCAG--VPGVGVPGAGIPVVPAGIPGAAYVPGVVSPEAAAAATAAK 356  
Db 260 PGGPFGPGVGVPGFAGVPGVGVPGAGIPVVPAGIPGAAGFAGVSPAAAAATAAK 319  
  
QY 357 YGARPFGVGGIPTYTCVAGGPGPGVGGVGGIPGVAGVPSVGGVPGVGGVSPVGAQ 416  
Db 320 YGARPFGVGGIPTYTCVAGGPGPGVGGVGGIPGVAGVPSVGGVPGVGGVSPVGAQ 379  
  
QY 417 AAAAATAAYKGYGTAAAAAATAAKAAQFGLVPGVGVAPGVGVAPGVGVGLAPGVG 476  
Db 380 AAAAATAAYKGYGTAAAAAATAAKAAQFGLVPGVGVAPGVGVAPGVGVGLAPGVG 439  
  
QY 477 VAPGVGVAPGVGVAPGVGGVAAAATAAKAAQFGLVPGVGVAPGVGVAPGVGVGL 536  
Db 440 VAPGVGVAPGVGVAPGVGGVAAAATAAKAAQFGLVPGVGVAPGVGVAPGVGVGL 499  
  
QY 537 GVGAGVPLGLGVAGVPGFAGVPGALAAATAAKAAYGAAVPGVGLGGVGGVPGVAG 596  
Db 500 GVGAGVPLGLGVAGVPGFAGVPGALAAATAAKAAYG--AVPGVGLGGVGGVPGVAG 558  
  
QY 597 PAAAAATAAKAAQFGLVGGAGLGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 656  
Db 559 PAAAAATAAKAAQFGLVGGAGLGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 618  
  
QY 657 GGVLGAGGQFPLGGVAAAPGFGLSPIPFPGACLGKACGRKRK 698  
Db 619 GGVLGAGGQFPLGGVAAAPGFGLSPIPFPGACLGKACGRKRK 660  
  
RESULT 19  
ADM03792  
ID ADM03792 standard; protein; 663 AA.  
XX AC  
XX ADM03792;  
XX DT  
XX 20-MAY-2004 (first entry)  
XX DE Human protein of the invention SEQ ID NO:2477.  
XX human; gene therapy; diagnostic marker; pharmaceutical.  
KW

XX Homo sapiens.  
OS  
XX EPI347046-A1.  
PN  
XX 24-SEP-2003.  
PD  
XX 12-APR-2002; 2002EP-00008400.  
PF  
XX 22-MAR-2002; 2002JP-00137785.  
PR  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
PA  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irle R, Iamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-723558/69.  
DR N-PSDB; ADM01349.  
DR  
XX New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.  
XX  
PS Claim 1; SEQ ID NO 2477; 305pp; English.  
XX  
CC The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention may have a use in gene  
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC protein sequence of the invention.  
XX  
SQ Sequence 663 AA;  
  
Query Match 89.4%; Score 3233.5; DB 7; Length 663;  
Best Local Similarity 90.8%; Pred. No. 8.5e-180;  
Matches 634; Conservative 0; Mismatches 3; Indels 61; Gaps 2;  
  
QY 1 GGVPCALPGGVPGGVFFYFAGLGGGALGGGKPLKVPVGGLAGLGGAGLGAFAVPT 60  
Db 27 GGVPCALPGGVPGGVFFYFAGLGGGALGGGKPLKVPVGGLAGLGG----- 76  
  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVVPGAGVKGVPVGL 120  
Db 77 -----AGAGLGGVPGVGGVSGAGAVVPGAGVKGVPVGL 115  
  
QY 121 PGVYVPGVLPGARFPGVGLPGVPTGAGVKKPKAPGVGGAFAGIPGVGPGQPGVPLGY 180  
Db 116 PGVYVPGVLPGARFPGVGLPGVPTGAGVKKPKAPGVGGAFAGIPGVGPGQPGVPLGY 175  
  
QY 181 PIKAPKLPGGYGLPYTTTKLPGYGGVPGVAGAKAGYPTGTGVPQAAAAAATAAKAF 240  
Db 176 PIKAPKLPGGYGLPYTTTKLPGYGGVPGVAGAKAGYPTGTGVPQAAAAAATAAKAF 235  
  
QY 241 GAGAGVLPVGGAGVPGVPGALPGTGGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 300  
Db 236 GAGAGVLPVGGAGVPGVPGALPGTGGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 295  
  
QY 301 PGFPGVVGVPVGGVPGVPGAGIPVVPAGIPGAAYVPGVVSPEAAAAATAAKAYCAR 360  
Db 296 PGFPGVVGVPVGGVPGVPGAGIPVVPAGIPGAAYVPGVVSPEAAAAATAAKAYCAR 355  
  
QY 361 PGVGVGGIPYTVGAGGFPFGVGGVGGIPGVAGVPSVGGVGGVGGVGGVGGVGGVGG 420  
Db 356 PGVGVGGIPYTVGAGGFPFGVGGVGGIPGVAGVPSVGGVGGVGGVGGVGGVGGVGG 415  
  
QY 421 AKAAKYGVTPEAAAAATAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG 480  
Db 421 AKAAKYGVTPEAAAAATAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG 480





so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

SQ Sequence 571 AA;

Query Match 79.4%; Score 2869; DB 3; Length 571;  
 Best Local Similarity 99.6%; Pred. No. 1e-158;  
 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGVPGAI PGVPGGV FYPGAGLGGALGPGGKPLKVPVGGLAGAGLGAFPAVT 60  
 Db 1 GGVPGAI PGVPGGV FYPGAGLGGALGPGGKPLKVPVGGLAGAGLGAFPAVT 60

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKPKVPGVGL 120  
 Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKPKVPGVGL 120

QY 121 PGVPGGVLPGARFPFGVGLPFGVPTGAGVKPKAPGVGGAFAGIPGVPGPGPGVPLGY 180  
 Db 121 PGVPGGVLPGARFPFGVGLPFGVPTGAGVKPKAPGVGGAFAGIPGVPGPGPGVPLGY 180

QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAA KAAAKF 240  
 Db 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAA KAAAKF 240

QY 241 GAGAAVLPGVGGAGVPGVPGAGIPVPGAGIPGAAVPGVSPPEAAAKAAKAAKYGAR 360  
 Db 241 GAGAAVLPGVGGAGVPGVPGAGIPVPGAGIPGAAVPGVSPPEAAAKAAKAAKYGAR 360

QY 301 PGFPGVGVPGAGVPGVPGAGIPVPGAGIPGAAVPGVSPPEAAAKAAKAAKYGAR 360  
 Db 301 PGFPGVGVPGAGVPGVPGAGIPVPGAGIPGAAVPGVSPPEAAAKAAKAAKYGAR 360

QY 361 PGVGVGGIPTYGVAGGFPFGVGVGIPGVAGVSPVGGVPGVGVGIPSPQAQAAA 420  
 Db 361 PGVGVGGIPTYGVAGGFPFGVGVGIPGVAGVSPVGGVPGVGVGIPSPQAQAAA 420

QY 421 AKAAKYGVGTTPAAA KAAKAAKAAQFGLVPGVGVAPGVGVAPGVGVGLAPGVGVAPG 480  
 Db 421 AKAAKYGVGTTPAAA KAAKAAKAAQFGLVPGVGVAPGVGVAPGVGVGLAPGVGVAPG 480

QY 481 VGAVPGVGVAPGIPGPGVAAAAAKAAKAAQFGLVPGVGVAPGVGVGLAGIPGLGVGVG 540  
 Db 481 VGAVPGVGVAPGIPGPGVAAAAAKAAKAAQFGLVPGVGVAPGVGVGLAGIPGLGVGVG 540

QY 541 GVPGLGVAGVPGF 554  
 Db 541 GVPGLGVAGVPGF 554

RESULT 23

AA569135

ID AA569135 standard; protein; 515 AA.

XX

AC AA569135;

XX

DT 30-MAY-2000 (first entry)

XX

Amino acid sequence of a human tropoelastin derivative.  
 Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

OS Homo sapiens.

XX WO200004043-A1.

XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-AU000580.

XX 17-JUL-1998; 98AU-00004723.

XX (UNSY) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 2000-182399/16.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.

XX Disclosure; Page 131-133; 136pp; English.

XX The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

XX Sequence 515 AA;

Query Match 74.1%; Score 2680; DB 3; Length 515;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-148;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGAI PGVPGGV FYPGAGLGGALGPGGKPLKVPVGGLAGAGLGAFPAVT 60

Db 1 GGVPGAI PGVPGGV FYPGAGLGGALGPGGKPLKVPVGGLAGAGLGAFPAVT 60

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKPKVPGVGL 120

Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKPKVPGVGL 120

QY 121 PGVPGGVLPGARFPFGVGLPFGVPTGAGVKPKAPGVGGAFAGIPGVPGPGVPLGY 180

Db 121 PGVPGGVLPGARFPFGVGLPFGVPTGAGVKPKAPGVGGAFAGIPGVPGPGVPLGY 180

QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAA KAAAKF 240

Db 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAA KAAAKF 240

QY 241 GAGAAVLPGVGGAGVPGVPGAGIPGIPGIGIAGVTPAAAAA KAAKAAKYGAAAGLVPGG 300

Db 241 GAGAAVLPGVGGAGVPGVPGAGIPGIPGIGIAGVTPAAAAA KAAKAAKYGAAAGLVPGG 300

CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
xx  
SQ Sequence 864 AA;  
  
Query Match 64.1%; Score 2315.5; DB 7; Length 864;  
Best Local Similarity 60.4%; Pred. No. 1.8e-126;  
Matches 529; Conservative 26; Mismatches 102; Indels 219; Gaps 34;  
  
Qy 1 GGVPGLPGGVPGGVFPYAGL-CALGGALPGGKPLKP-----VPGGLAGAGL 49  
Db 30 GGVPGLPGGVPGGVFPYAGLIGGLGGALPGGKPKPGAGLLGAFAGPGGLGGAGP 89  
  
Qy 50 GAGLGAPPAVTFPGALVPGGVADAAAYK-AAKAGAGLGGVPGV----- 92  
Db 90 GAGLSY--ASRPGGLVPGGGAGAAAYKAAKAGAGLGGIGGVPGGVGVPGAVGVG 147  
  
Qy 93 -----GGLGVSAAGVVPQAGV---KPGKVPGLPGVVPGLP---GARF 134  
Db 148 GVPAGVGGIGGIGGLGVSTGAVPQLGAGVGAGKPGKVPGLPGVVPGLPGTGARF 207  
  
Qy 135 PGVGLPGVPTGAGVTKAP-GVGGAFAPIGVPGFPGPQGVPLGPIKAPLPGVGL 193  
Db 208 PGVGLPGVPTGTGKAVKVPGGGGAFSGIPGVFGQQQPGVPLGPIKAPLPGVGL 267  
  
Qy 194 PYTTGKLPVPGGVGAGAACAGVPTGTGVPQAAAAAAKAAKAFGAGAGVLPVGG 253  
Db 268 PYTNKLPY-----GVAGAGKAGTPTGTGVSQ-AAVAAKAAKYGAGGGVLPVGG 321  
  
Qy 254 AGVPGVPGAIPIGIGIAGVGTAAAAAAKAAKAGLPGGPGFPGVVPVGA 313  
Db 322 GGI PGAGAIPIGIGITAGTFAAAAAKAAKAAKAGAGLPGGPGF-----VRVPGA 376  
  
Qy 314 GVPVGVPGV-----AGIPVPGAGIPGAIV---PGVSPAAKAAKAAKAAK 357  
Db 377 GIPVGI PGVGGIPGVGGIPGVGGIPGVGGIPGVGGIPGVGGIPGVGGIPGV 436  
  
Qy 358 GARPVGVGGIPTVGVGAGGPGFGV----- 385  
Db 437 GARGGV---GIPTVGVGAGGPGFGVGGAGAGLGGASQAAAAAAKAAKYGAGGAGTGG 493  
  
Qy 386 -----GGIPGV--AGVP-----SVGGVPGVPGVPGVISPAAKAAKAAK 427  
Db 494 LVPGAVPGALPGAVFGALPGAVPGALPGAVPGVPGTGGVPGAG-----TPAAAA 542  
  
Qy 428 VGTAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 487  
Db 543 -----AAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 592  
  
Qy 488 GVAPG-IGPGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 546  
Db 593 GLVPGDLGGATPAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 650  
  
Qy 547 VGAGVPGF--GAVPGALAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 590  
Db 651 AGAGVPGFAGAVPGSLAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 710  
  
Qy 591 GUVGAPAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 630  
Db 711 GVAGGAP-AAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 769  
  
Qy 631 -VPGVGGIGIPAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 684  
Db 770 VIPGAVGLGVSPAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 828

QY	685	-----GGACLGKACGKRRK 698
Db	829	GLGVGKPKPYGGALCALGYGGGCGKSCGKRRK 864
RESULT 25		
AA88422		
ID	AA88422	standard; protein; 472 AA.
AC	AA88422;	
DT	23-MAY-2001	(first entry)
XX		Human membrane or secretory protein clone PSEC0191.
DE		Human; secretory protein; membrane protein; vaccine; gene therapy;
KW		rheumatoid arthritis; diabetes.
XX		Homo sapiens.
OS		
PN	EP1067182-A2.	
XX		
PD	10-JAN-2001.	
XX		
PF	07-JUL-2000;	2000EP-00114090.
XX		
PR	08-JUL-1999;	95JP-00194179.
PR	11-JAN-2000;	2000JP-00118775.
PR	02-MAY-2000;	2000JP-00183766.
XX		
PA	(HELI-) HELIX RES INST.	
XX		
PI	Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;	
XX		
DR	WPI; 2001-093989/11.	
DR	N-PSDB; AAF93849.	
XX		
PT	Nucleic acids encoding secretory proteins/membrane proteins, useful in	
PT	gene therapy or as candidate target molecules in drug development.	
XX		
PS	Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.	
XX		
CC	This invention relates to nucleic acid sequences AAF93744 - AAF93916	
CC	which encode human secretory or membrane proteins represented by AAF88317	
CC	- AAF88419. Included in the invention are primers AAF93917 - AAF94295 and	
CC	AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the	
CC	invention. The invention also includes methods for the production of	
CC	antibodies directed against the proteins, and cDNA sequences, which can	
CC	be used in vaccines. The polynucleotide sequences can be used in gene	
CC	therapy. The polynucleotide sequences and the proteins they encode may be	
CC	used in the prevention, treatment and diagnosis of diseases associated	
CC	with inappropriate secretory protein/membrane protein expression. The	
CC	nucleic acids and complementary sequences may also be used as DNA probes	
CC	in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect	
CC	and quantitate the presence of similar nucleic acid sequences in samples.	
CC	They may also be used to study the expression and function of secretory	
CC	proteins/membrane polypeptides and their role in metabolism. The	
CC	polypeptides may be used as antigens in the production of antibodies	
CC	against them and in assays to identify modulators (agonists and	
CC	antagonists) of expression and activity. The antibodies and antagonists	
CC	may also be used as therapeutic agents to down regulate expression and	
CC	activity. The antibodies may also be used as diagnostic agents for	
CC	detecting the presence of the polypeptides in samples (e.g. by enzyme	
CC	linked immunosorbant assay (ELISA). Examples of diseases which may be	
CC	treated include rheumatoid arthritis and diabetes	
XX		
SQ	Sequence 472 AA;	
Query Match	46.4%;	Score 1679; DB 4; Length 472;
Best Local Similarity	60.5%;	Pred. No. 8.9e-90;
Matches	356; Conservative	3; Mismatches 3; Indels 226; Gaps 5;
QY	1	GGVPGALPGVPGVFPYGGALGCGGALPGCGKLPKPVPGGLAGAGLGAFFAVT 60







[illegible]

RESULT 28

RESULI 2  
AAR80252

AAR60252  
ID AAR

XX  
AFAC

AC AAR

XXX

DT 17-

XX

DE POLY

XX

KW Fib:

KW  
pol;

XX 8

Synt  
OS

XX

PH	Key	Location/Qualifiers
FI	Peptide	1. .64
FT		/note= "polymer repeat block sequence"
XX		
XX		
XX	WC9524478-A1.	
XX		
XX		
PD	14-SEP-1995.	
XX		
PF	10-MAR-1995;	9SWO-US002772.
XX		
PR	11-MAR-1994;	94US-00212237.
XX		
XX		
PA	(PROT-) PROTEIN POLYMER TECHNOLOGIES INC.	
XX		
XX		
PI	Cappello J;	
XX		
XX		
DR	WPI; 1995-328270/42.	

Protein polymer comprising alternating blocks of fibroin and elastin units - used to form a device e.g. a suture to keep separated viable tissue together.

Example 1; Page 25-27; 46pp; English.

The sequences represented by AAR80251-R80257 are polymers constructed of repeating blocks of fibroin-like (see AAR80249) and elastin-like (see AAR80250) units. This sequence contains 13 repeats of a block consisting of 8 elastin-like repeats followed by 4 fibroin-like repeats. The DNA sequences encoding these polymers were inserted into plasmids which were used to transform *E. coli* strain EC3. The polymers could then be isolated from the fermented strains by standard centrifugation techniques. The polymers are used to form a device (such as a suture, pin, thread, gel or film) to keep separated viable tissue together. By varying the the ratio of the two repetitive units, and by altering the lengths of the blocks of each of them, the tensile properties of the polymer can be altered moderately. By reducing the number of repeating units of this sequence, or by increasing the number of units of the elastin like repeat, a faster rate of resorption can be achieved. Of the polymers, SELP0 (see AAR80251) had the fastest resorption rate. The SELP4 (see AAR80255) and SELP5 (see AAR80256) polymers showed no resorption after seven weeks. The other three polymers showed intermediate resorption. No data was given for SELP6 (see AAR80257).

Sequence 832 AA:

Query Match	31.8%;	Score 1150.5;	DB 2;	Length 832;
Best Local Similarity	44.5%;	Pred. No. 6.4e-59;		
Matches 345:	Conservative	48.	Mismatches 228.	Indels 155.

[illegible]

Fibroin; elastin; repeat sequence; suture; thread; pin; gel; silk; polymer; E.coli; EC3.  
Synthetic.







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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 10.014 Seconds  
(without alignments)  
1755.321 Million cell updates/sec

Title: US-09-743-818A-72

Perfect score: 253

Sequence: 1 AAGLAGIGELGVGVGVPG.....LGVGAGVPGAGAGGVRR 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	253	100.0	216	2	AAY01310 Human tro
2	253	100.0	730	2	AAW46315 Human ela
3	253	100.0	731	3	AAY69068 Amino aci
4	253	100.0	731	4	AAB66657 Human ela
5	253	100.0	731	6	ABU08725 Human ela
6	253	100.0	731	7	ADL96420 Human ela
7	253	100.0	733	2	AAW56653 Synthetic
8	253	100.0	733	2	AAY01301 Amino aci
9	253	100.0	757	7	ABG75223 Human tro
10	253	100.0	757	7	ADP65160 Human ela
11	212	83.8	183	3	AAY01311 Human tro
12	212	83.8	183	3	AAY69138 Human tro
13	212	83.8	617	7	ADB64761 Amino aci
14	212	83.8	660	2	ADM03792 Human tro
15	212	83.8	663	7	ADM03792 Human tro
16	212	83.8	692	7	ADE40134 Human tro
17	212	83.8	698	2	AAY01302 Human tro
18	212	83.8	698	3	AAY69069 Human tro
19	212	83.8	711	7	ADE40132 Human tro
20	212	83.8	712	3	AAW08630 Amino aci
21	212	83.8	730	3	AAW08631 Fusion pr
22	212	83.8	730	5	AAW017360 Human ela
23	212	83.8	730	8	ADQ19747 Human sof
24	212	83.8	870	7	ADE08527 Novel pro
25	208	82.2	472	4	AAB88422 Human mem

26	189	74.7	571	3	AAY69071	Aay69071 Amino aci
27	181	71.5	864	7	ADES6670	Ade56670 Rat Prote
28	159	62.8	34	1	AAP71455	Aap71455 Sequence
29	149	58.9	60	5	ABP53469	Abp53469 SELP9K DN
30	149	58.9	64	2	AAR80339	Aar80339 PPAS SELP
31	149	58.9	64	2	AAR80338	Aar80338 Protein p
32	149	58.9	64	2	AAR80340	Aar80340 PPAS SELP
33	149	58.9	64	2	AAW09211	Aaw09211 SELP8 mon
34	149	58.9	64	2	AAW09212	Aaw09212 SELP8 mon
35	149	58.9	64	2	AAW53538	Aaw53538 Amino aci
36	149	58.9	64	2	AAW49726	Aaw49726 SELP8K mo
37	149	58.9	64	2	AAW49725	Aaw49725 SELP8 mon
38	149	58.9	64	2	AAW49727	Aaw49727 SELP8E mo
39	149	58.9	64	3	AAW51881	Aaw51881 Plasmid p
40	149	58.9	64	5	ABG31411	Abg31411 SELP8K mo
41	149	58.9	64	5	ABP53464	Abp53464 SELP8 DNA
42	149	58.9	64	7	ABW01626	Abw01626 SELP8 mon
43	149	58.9	64	7	ABW01627	Abw01627 SELP8K mo
44	149	58.9	217	2	AAR80347	Aar80347 Protein p
45	149	58.9	223	2	AAR80348	Aar80348 Protein p
46	149	58.9	281	2	AAW49736	Aaw49736 Protein p
47	149	58.9	287	2	AAW49737	Aaw49737 Protein p
48	149	58.9	312	5	ABP53480	Abp53480 Protein p
49	149	58.9	378	2	AAW09219	Aaw09219 SELP8K po
50	149	58.9	378	2	AAW53545	Aaw53545 Amino aci
51	149	58.9	378	3	AAW51889	Aaw51889 Plasmid p
52	149	58.9	378	5	ABG31419	Abg31419 SELP8K pr
53	149	58.9	378	7	ABW01635	Abw01635 Plasmid p
54	149	58.9	696	5	ABP53470	Abp53470 SELP9K re
55	149	58.9	696	5	ABP53482	Abp53482 Protein p
56	149	58.9	696	8	ADK51955	Adk51955 Repeat pr
57	149	58.9	768	5	ABP53481	Abp53481 Protein p
58	149	58.9	768	5	ABP53466	Abp53466 SELP8 rel
59	149	58.9	877	2	AAR80335	Aar80335 Protein p
60	149	58.9	877	2	AAW49724	Aaw49724 Protein p
61	149	58.9	884	2	AAR80341	Aar80341 Protein p
62	149	58.9	884	2	AAW09213	Aaw09213 SELP8K po
63	149	58.9	884	2	AAW53541	Aaw53541 Expected
64	149	58.9	884	2	AAW49728	Aaw49728 SELP8K po
65	149	58.9	884	3	AAW51882	Aaw51882 Plasmid p
66	149	58.9	884	5	ABG31412	Abg31412 SELP8K po
67	149	58.9	884	7	ABW01628	Abw01628 Plasmid p
68	149	58.9	968	5	AAE18320	Aae18320 Silk elas
69	149	58.9	1002	2	AAW09218	Aaw09218 SELP8K po
70	149	58.9	1002	2	AAW53544	Aaw53544 Amino aci
71	149	58.9	1002	2	AAW51888	Aaw51888 Plasmid p
72	149	58.9	1002	5	ABG31418	Abg31418 SELP8K pr
73	149	58.9	1011	3	ABW01634	Abw01634 Plasmid p
74	149	58.9	1011	5	ABG69277	Abg69277 SELP8K pr
75	149	58.9	1011	5	ABG69277	Abg69277 SELP8K pr
76	149	58.9	1011	7	ABG69277	Abg69277 SELP8K pr
77	149	58.9	1170	2	AAW26351	Aaw26351 SELP8K pr
78	149	58.9	1170	2	AAW53527	Aaw53527 Amino aci
79	149	58.9	1412	2	AAW53519	Aaw53519 Amino aci
80	149	58.9	1413	1	AAW82957	Aaw82957 EBSI prot
81	149	58.9	1413	2	AAW41008	Aaw41008 EBSI mult
82	149	58.9	1413	2	AAW26343	Aaw26343 EBSI synt
83	149	58.9	1463	5	ABG69268	Abg69268 EBSI prot
84	149	58.9	1465	7	ABG69268	Abg69268 EBSI prot
85	149	58.9	1465	7	ABG69268	Abg69268 EBSI prot
86	149	58.9	1465	7	ABG69268	Abg69268 EBSI prot
87	149	58.9	2055	1	AAW82960	Aaw82960 SELP2 pro
88	149	58.9	2055	2	AAW41011	Aaw41011 SELP2 mul
89	149	58.9	2055	2	AAW26346	Aaw26346 SELP2 syn
90	149	58.9	2055	2	AAW53522	Aaw53522 Amino aci
91	149	58.9	2055	5	AAW78281	Aaw78281 SELP2 ami
92	149	58.9	2055	5	ABG69271	Abg69271 Silk/Elas
93	149	58.9	2055	7	ABG69271	Abg69271 Silk/Elas
94	149	58.9	2257	1	AAW82961	Aaw82961 SELP3 pro
95	149	58.9	2257	2	AAW41012	Aaw41012 SELP3 mul
96	149	58.9	2257	2	AAW26347	Aaw26347 SELP3 syn
97	149	58.9	2257	3	AAW53523	Aaw53523 Amino aci
98	149	58.9	2257	5	ABG69272	Abg69272 Silk/Elas

99 149 58.9 2257 7 ADE44977 Ade44977 Recombina  
100 148.5 58.7 65 3 AAY51880 Aay51880 Crosslink

## ALIGNMENTS

RESULT 1  
AAV01310  
ID AAY01310 standard; protein; 216 AA.  
XX AC AAY01310;  
XX  
XX 07-JUN-1999 (first entry)  
XX  
XX Human tropoelastin derivative SHEL26-36.  
XX  
XX Tropoelastin; hTPE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO9903886-A1.  
XX  
XX 28-JAN-1999.  
XX  
XX 17-JUL-1998; 98WO-AU000564.  
XX  
XX 18-JUL-1997; 97AU-00008117.  
XX  
XX (UNSY ) UNIV SYDNEY.  
XX  
XX Weiss AS;  
XX  
XX WPI; 1999-132162/11.  
XX  
XX New derivatives of human tropoelastin - with elastin-like or  
PT macromolecular binding properties, useful e.g. as surgical implants.  
XX  
XX Claim 35; Page 11; 82pp; English.  
XX  
XX The invention relates to a derivative or variant of human tropoelastin  
CC (hTPE) having elastin-like and/or macromolecule (specifically  
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
CC comprising the nucleic acids encoding the variants or derivatives are  
CC used to produce the proteins recombinantly. The tropoelastin derivatives  
CC or hybrid proteins containing the derivatives are useful in medical,  
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
CC products. The hybrid protein have controllable GAG-binding properties,  
CC depending on presence or absence of a specific fragment, designated  
CC peptide 26A, from hTPE. The present sequence represents a human  
CC tropoelastin derivative SHEL26-36  
XX  
XX Sequence 216 AA;  
SQ

Query Match 100.0%; Score 253; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 2.1e-17; Indels 0; Gaps 0;  
Matches 49; Conservative 0; Mismatches 0;

QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 49  
|||||  
Db 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 49  
|||||

RESULT 2  
AAW46315  
ID AAW46315 standard; protein; 730 AA.  
XX AC AAW46315;  
XX

23-JUL-1998 (first entry)  
XX Human elastin containing non-natural polypeptide MFU-1 sequence.  
DE  
XX  
XX MFU-1; minimal functional unit; elastin; human; fibrous protein;  
KW beta-sheet; coating; wound dressing.  
XX  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 374. .499  
FT Protein /note= "MFU-1 polypeptide"  
FT  
XX  
XX WO9805685-A2.  
XX  
XX 12-FEB-1998.  
XX  
XX 07-AUG-1997; 97WO-CA000560.  
XX  
XX 07-AUG-1996; 96US-0023552P.  
XX  
XX 07-AUG-1997; 97US-00911364.  
XX  
XX (PROT-) PROTEIN SPECIALTIES LTD.  
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.  
XX  
XX Rothstein A, Keeley FW, Rothstein SJ;  
XX  
XX WPI; 1998-145551/13.  
XX  
XX New non-natural polypeptide with multiple beta-sheet, beta-turn  
PT structures - particularly based on human elastin, useful for coating  
PT prostheses, as wound dressings, etc., allows ingrowth of cells.  
XX  
XX Claim 5; Fig 1B; 39pp; English.  
XX  
XX This represents the human elastin sequence containing the minimal  
CC functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a  
CC polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is  
CC not a naturally occurring fibrous protein. Each beta-sheet structure has  
CC 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at  
CC least 1 amino acid that can take part in crosslinking. The polypeptide  
CC can also be derived from the sequences of animal elastin, lamprin and  
CC spider silk protein. The MFU polypeptides are self-aligning peptides  
CC having the same primary structure as part of a natural fibrous protein.  
CC They are used to coat prostheses made of animal or synthetic material or  
CC metal, particularly for use as blood vessel or heart valve replacements,  
CC wound or burn dressings, or stents. They can be used in cosmetic, elastic  
CC or high-tensile strength materials, e.g. ropes or parachute cord.  
CC Prostheses based on the MFU allow penetration of endothelial cells, so  
CC become permanent, living, tissue replacements. The MFU polypeptides have  
CC better biocompatibility than known elastin-based materials. They are well  
CC defined, homogeneous material and are easier to manipulate and produce  
CC than full-length elastins. They are non-thrombogenic and non-immunogenic.  
CC Materials can be made from 2 or more different MFU polypeptides to allow  
CC properties to be tailored for particular applications, e.g. combining the  
CC high extensibility of elastin and the high tensile strength of spider  
CC silk protein  
XX  
XX Sequence 730 AA;  
SQ

Query Match 100.0%; Score 253; DB 2; Length 730;  
Best Local Similarity 100.0%; Pred. No. 6.4e-17;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 49  
|||||  
Db 516 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 564  
|||||

RESULT 3  
AAY69068  
ID AAY69068 standard; protein; 731 AA.  
XX

AC AAY69068;  
 DT 30-MAY-2000 (first entry)  
 DE Amino acid sequence of a human tropoelastin splice form.  
 DE Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Cleavage-site 441..442  
 FT Cleavage-site 503..504  
 FT Cleavage-site 515..516  
 FT Cleavage-site 564..565  
 XX WO200004043-A1.  
 XX 27-JAN-2000.  
 XX 19-JUL-1999; 99WO-AU000580.  
 XX 17-JUL-1998; 98AU-00004723.  
 XX (UNSY ) UNIV SYDNEY.  
 XX Weiss AS;  
 XX WPI; 2000-182399/16.  
 XX N-PSDB; AAZ61146.  
 XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.  
 XX Disclosure; Page 107-109; 136pp; English.  
 XX The present sequence represents a human tropoelastin splice form. The  
 CC specification describes tropoelastin derivatives, in which a subsequence  
 CC has been mutated so that susceptibility to proteolysis is reduced or  
 CC eliminated, or a subsequence has been inserted so that susceptibility to  
 CC proteolysis is increased. The derivatives have with reduced  
 CC susceptibility, and can be used where the wild-type protein would be  
 CC degraded too easily, e.g. in contact with serum or wound exudate. The  
 CC tropoelastin derivatives provide competitive inhibition of protease  
 CC activity. The tropoelastin derivatives, and other polypeptides containing  
 CC tropoelastin derivative-derived protease-susceptibility sites, are useful  
 CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand  
 CC lotions), as bulking agents and for inducing chemotaxis. They are also  
 CC useful for proliferation or growth inhibition, particularly of smooth  
 CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,  
 CC chondrocytes and platelets. Peptidomimetics that mimic the protease  
 CC cleavage site in tropoelastin derivatives are competitive inhibitors of  
 CC the protease, and are used for protecting against lung damage caused by  
 CC elastin, for inhibiting or controlling localized growth of cancers or  
 CC metastases, or to limit protease activity that causes blood clotting  
 XX Sequence 731 AA;  
 Query Match 100.0%; Score 253; DB 3; Length 731;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGPGLVGAGVPGLVGAGVPGFAGADEGVRR 49  
 Db 516 AAAGLGAGIPGLGVGVGPGLVGAGVPGLVGAGVPGFAGADEGVRR 564  
 RESULT 4  
 AAB66657  
 ID AAB66657 standard; protein; 731 AA.  
 XX

AC AAB66657;  
 DT 05-APR-2001 (first entry)  
 DE Human elastin protein without signal peptide.  
 DE Minimal function unit; MFU; human; elastin prosthetic.  
 KW Homo sapiens.  
 OS WO200100666-A2.  
 XX 04-JAN-2001.  
 XX 29-JUN-2000; 2000WO-US017829.  
 XX 29-JUN-1999; 99US-00340736.  
 XX (PROT-) PROTEIN SPECIALTIES LTD.  
 XX (HSCR-) HSC RES & DEV LP.  
 XX Rothstein A, Keeley F, Rothstein S, Stahl R;  
 XX WPI; 2001-102886/11.  
 XX Novel polypeptides that comprise three beta-sheet/beta-turn structures  
 PT and are not naturally occurring fibrous protein, used to produce  
 PT prosthesis suitable for implantation into humans, and cosmetic materials.  
 XX Claim 1; Fig 1; 39pp; English.  
 XX The present invention relates to a minimal functional unit (MFU) of human  
 CC elastin polypeptide. This protein is useful in a cosmetic material or a  
 CC prosthetic material such as prosthesis for blood vessel replacements, for  
 CC heart valve replacement, tissue replacement, for covering burns, for  
 CC covering wounds and stents  
 XX Sequence 731 AA;  
 Query Match 100.0%; Score 253; DB 4; Length 731;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGPGLVGAGVPGLVGAGVPGFAGADEGVRR 49  
 Db 516 AAAGLGAGIPGLGVGVGPGLVGAGVPGLVGAGVPGFAGADEGVRR 564  
 RESULT 5  
 AAB66657  
 ID AAB66657 standard; protein; 731 AA.  
 XX ABU08725;  
 XX 25-JUN-2003 (first entry)  
 DE Human elastin mature protein.  
 XX Human; elastin; minimal functioning unit; MFU;  
 KW beta-sheet/beta-turn structure; fibrous protein; prosthesis;  
 KW blood vessel replacement; heart replacement valve; burn; wound; lamprin;  
 KW spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;  
 KW platelet activation inhibitor; non-thrombogenic; cell infiltration;  
 KW non-immunogenic; biocompatible; high tensile strength; elasticity;  
 XX plasticity.  
 XX Homo sapiens.  
 XX US6489446-B1.  
 XX 03-DEC-2002.  
 XX 29-JUN-1999; 99US-00340736.

XX 07-AUG-1996; 96US-0023522P.  
PR 07-AUG-1997; 97US-00911364.  
XX (HSCR-) HSC RES & DEV LP.  
PA (PROT-) PROTEIN SPECIALTIES LTD.  
XX Rothstein A, Keeley F, Rothstein S;  
XX WPI; 2003-391056/37.  
XX Novel polypeptide useful in prosthesis, has a secondary structure  
PT characterized by three beta-sheet/beta-turn structures, and is not a  
PT naturally occurring fibrous protein.  
XX Claim 1; Fig 1B; 21pp; English.  
XX The invention describes a polypeptide (I) comprising a minimal  
CC functioning unit (MFU) which is present in the sequence of human elastin  
CC and comprised of at least three beta-sheet/beta-turn structures, and at  
CC least one amino acid residue that participates in cross-linking, and not  
CC a naturally occurring fibrous protein. The MFU material can be used to  
CC construct human elastin-like prostheses such as tubes for blood vessel  
CC replacement, heart replacement valves and sheets for other uses such as  
CC burns or wounds to promote healing. MFUs can be co-aggregated with other  
CC proteins, for e.g. collagen, to provide prosthesis material that  
CC resembles the natural structural materials of the body. MFUs modeled on  
CC lamprin and other fibrous proteins e.g. spider silk, can be used to make  
CC a variety of materials, for a number of different applications, for e.g.  
CC in cords and ropes for use in parachutes and in cosmetics. Coating  
CC synthetic prosthesis with MFUs modeled on human elastin significantly  
CC inhibits platelet binding and activation. The human-like MFU material is  
CC more biocompatible than other elastin-containing materials. In contrast  
CC to solubilised fragments of elastin used before, an MFU is a single  
CC peptide of defined composition. The MFU is considerably smaller than the  
CC parent protein, simpler in structure, easier to produce or express in  
CC practical purposes. Like other elastin preparations, the MFU is non-  
CC thrombogenic and provides a friendly environment for cell infiltration.  
CC Being composed entirely of a human elastin sequence, MFU is non-  
CC immunogenic, thus providing a truly biocompatible material. MFUs modeled  
CC on lamprin and other fibrous proteins can be used to make a variety of  
CC materials having high tensile strength, elasticity and plasticity of  
CC their parent proteins. This is the amino acid sequence of mature human  
CC elastin on which the MFU peptides of the invention are based  
XX Sequence 731 AA;  
SQ Query Match 100.0%; Score 253; DB 6; Length 731;  
Best Local Similarity 100.0%; Pred. No. 6.4e-17;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 49  
Db 516 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 564  
RESULT 6  
ADL96420  
ID ADL96420 standard; protein; 731 AA.  
XX ADL96420;  
XX 20-MAY-2004 (first entry)  
XX Human elastin protein fragment.  
XX fibrous protein; prosthesis; elastin; lamprin; spider silk protein;  
KW blood vessel; wound; burn healing; collagen.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH

FT Region 19. .160  
FT /note= "region specifically claimed in claim 6"  
FT 188. .367  
FT /note= "region specifically claimed in claim 6"  
FT 374. .499  
FT /note= "region specifically claimed in claim 6"  
FT 607. .717  
FT /note= "region specifically claimed in claim 6"  
XX US2003166846-A1.  
PN 04-SEP-2003.  
XX 28-SEP-2001; 2001US-00964562.  
XX 07-AUG-1996; 96US-0023522P.  
PR 07-AUG-1997; 97US-00911364.  
PR 29-JUN-1999; 99US-00340736.  
XX (ROTH/) ROTHSTEIN A.  
XX (KEEL/) KEELLEY F.  
XX (ROTH/) ROTHSTEIN S.  
XX Rothstein A, Keeley F, Rothstein S;  
XX WPI; 2003-898105/82.  
XX Polypeptide for constructing human elastin-like prostheses such as tubes  
PT for blood vessel replacement and sheets for other uses such as wound or  
PT burn healing, comprises three beta sheets and three beta turns.  
XX Claim 5; Fig 1B; 17pp; English.  
XX This invention describes a polypeptide that comprises three beta  
CC sheet/beta turn structures and that is not a naturally occurring fibrous  
CC protein. The invention also describes a prosthesis comprising an animal,  
CC metal or synthetic material, where the surface is coated with the  
CC polypeptide, a cosmetic material comprising the polypeptide, an elastic  
CC material comprising the polypeptide, a high tensile strength material  
CC comprising the polypeptide, a material comprising two or more  
CC polypeptides selected from (a) a polypeptide consisting essentially of a  
CC portion of the polypeptide comprising at least three beta sheet/beta turn  
CC structures, (b) a polypeptide consisting essentially of a portion of the  
CC amino acid sequence of an animal elastin comprising at least three beta  
CC sheets/beta turns, (c) a polypeptide consisting essentially of a portion  
CC of lamprin comprising at least three beta sheets/beta turns, and (d) a  
CC polypeptide consisting essentially of a spider silk protein comprising at  
CC least three beta sheets/beta turns, a polypeptide having the primary  
CC structure of a portion of a naturally occurring fibrous protein and a  
CC secondary structure comprising at least three beta sheets/beta turns, a  
CC where each of the beta sheet/beta turn structures comprises from 3 to  
CC about 7 amino acids and the polypeptide is not a naturally occurring  
CC fibrous protein. The minimal functional unit (MFU) of the invention is  
CC useful to construct human elastin-like prostheses such as wound or burn  
CC vessel replacement and sheets for other uses such as wound or burn  
CC healing. Alternatively the MFU can be co-aggregated with other proteins,  
CC for example collagen, to provide prosthesis material that resembles the  
CC natural structural materials of the body. The MFU based material is  
CC subject to infiltration of cells growing in the patient, including  
CC endothelial cells, and the prosthesis can become a permanent living  
CC tissue replacement. The material is more biocompatible than other elastin  
CC -containing materials proposed for prostheses.  
XX Sequence 731 AA;  
SQ Query Match 100.0%; Score 253; DB 7; Length 731;  
Best Local Similarity 100.0%; Pred. No. 6.4e-17;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 49  
Db 516 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGAGADEGVRR 564



RESULT 7  
 AAR56653  
 ID AAR56653 standard; protein; 733 AA.  
 XX AC AAR56653;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 22-MAR-1995 (first entry)  
 XX DE Synthetic human tropoelastin (SHEL).  
 XX KW Tropoelastin; pharmaceutical; surgical dressing.  
 XX OS Synthetic.  
 XX PN WO9414958-A1.  
 XX PD 07-JUL-1994.  
 XX PF 16-DEC-1993; 93WO-AU000655.  
 XX PR 22-DEC-1992; 92AU-00006520.  
 XX PR 28-JUN-1993; 93AU-00009661.  
 XX PA (UNSY ) UNIV SYDNEY.  
 XX PI Weiss AS, Martin SL;  
 DR WPI; 1994-263633/32.  
 DR N-PSDB; AAQ70941.  
 XX Synthetic polynucleotide(s) - encode recombinant tropoelastins and variants.  
 XX PS Disclosure; Page 30; 77pp; English.  
 XX CC Human synthetic tropoelastin is susceptible to hydrolytic breakdown of the crosslinks. Such material may be useful in e.g. surgical applications, where the gradual loss of material over time is intended. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 733 AA;  
 Query Match 100.0%; Score 253; DB 2; Length 733;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 49  
 Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 566  
 RESULT 8  
 AAY01301  
 ID AAY01301 standard; protein; 733 AA.  
 XX AC AAY01301;  
 XX DT 07-JUN-1999 (first entry)  
 XX DE Amino acid sequence of synthetic human tropoelastin SHEL.  
 XX KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN WO9903886-A1.  
 XX PD 28-JAN-1999.  
 Query Match 100.0%; Score 253; DB 2; Length 733;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 49  
 Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 566  
 RESULT 9  
 ABG75223  
 ID ABG75223 standard; protein; 757 AA.  
 XX AC ABG75223;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Human tropoelastin protein.  
 XX KW Human; tropoelastin; elastin; body vessel occlusion; stenosis; vascular smooth muscle cell; elastin signaling; vasotrophic.  
 XX OS Homo sapiens.  
 XX PN WO2003082203-A2.  
 XX PD 09-OCT-2003.  
 XX PF 27-MAR-2003; 2003WO-US009391.  
 XX PR 27-MAR-2002; 2002US-0368084P.  
 XX PA (UTAH ) UNIV UTAH RES FOUND.  
 XX PI Li DY, Karnik S;  
 DR WPI; 2003-833516/77.  
 Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or

XX PF 17-JUL-1998; 98WO-AU000564.  
 XX PR 18-JUL-1997; 97AU-00008117.  
 XX PA (UNSY ) UNIV SYDNEY.  
 XX PI Weiss AS;  
 XX DR WPI; 1999-132162/11.  
 XX DR N-PSDB; AAX27704.  
 XX PT New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.  
 XX PS Disclosure; Fig 1; 82pp; English.  
 XX CC The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the amino acid sequence of the synthetic human tropoelastin SHEL  
 XX SQ Sequence 733 AA;  
 Query Match 100.0%; Score 253; DB 2; Length 733;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 49  
 Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 566  
 RESULT 9  
 ABG75223  
 ID ABG75223 standard; protein; 757 AA.  
 XX AC ABG75223;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Human tropoelastin protein.  
 XX KW Human; tropoelastin; elastin; body vessel occlusion; stenosis; vascular smooth muscle cell; elastin signaling; vasotrophic.  
 XX OS Homo sapiens.  
 XX PN WO2003082203-A2.  
 XX PD 09-OCT-2003.  
 XX PF 27-MAR-2003; 2003WO-US009391.  
 XX PR 27-MAR-2002; 2002US-0368084P.  
 XX PA (UTAH ) UNIV UTAH RES FOUND.  
 XX PI Li DY, Karnik S;  
 DR WPI; 2003-833516/77.  
 Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or

CC The invention relates to a novel method for diagnosing and analysing  
CC autoimmune disease or arthritides. The method comprises obtaining a  
CC patient sample containing mRNA, analysing gene expression using the mRNA  
CC that results in a gene expression signature of the mRNA, and using that  
CC gene expression signature to diagnose or analyse the autoimmune disease  
CC or arthritides in the patient, where gene expression of at least 60% of  
CC the genes correlates with that of the gene signature. The invention  
CC further comprises: a treatment of rheumatoid arthritis in a mammal  
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal; an  
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
CC efficacy of a candidate drug in vitro for the treatment of collagen-  
CC induced arthritis; and reducing the symptoms associated with the following  
CC induced arthritis. The compositions of the invention have the following  
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
CC methods and compositions of the present invention are useful for  
CC diagnosing and treating autoimmune disease or arthritides, such as  
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
CC immune disease caused by an infectious agent. This sequence represents a  
CC protein sequence relating to the genes used in the analysis and treatment  
CC of autoimmune diseases or arthritides. Note: This sequence is not shown  
CC in the specification. It has been supplied in an electronic format from  
CC WIPO.  
XX Sequence 757 AA;  
SQ Query Match 100.0%; Score 253; DB 7; Length 757;  
Best Local Similarity 100.0%; Pred. No. 6.7e-17; Indels 0; Gaps 0;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGAGIGPLGVGVGPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 49  
|||||  
DB 542 AAAGLGAGIGPLGVGVGPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 590  
|||||  
RESULT 11  
AAV01311  
ID AAV01311 standard; protein; 183 AA.  
XX AAV01311;  
XX 07-JUN-1999 (first entry)  
DT Human tropoelastin derivative SHEL26-36 (excluding exon 26A product).  
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
XX Homo sapiens.  
OS Synthetic.  
XX WO9903886-A1.  
PN 28-JAN-1999.  
PD 17-JUL-1998; 98WO-AU000564.  
PF 18-JUL-1997; 97AU-00008117.  
PR (UNSY ) UNIV SYDNEY.  
XX Weiss AS;  
PI WPI; 1999-132162/11.  
XX New derivatives of human tropoelastin - with elastin-like or  
PT macromolecular binding properties, useful e.g. as surgical implants.  
XX Claim 39; Page 11; 82pp; English.

PT preventing stenosis.  
XX Claim 24; Page 138-141; Opp; English.  
XX The present invention relates to the use of an agent that promotes  
CC elastin signaling in smooth muscle cells for decreasing or preventing  
CC occlusion of a body vessel by smooth muscle cells, decreasing vascular  
CC obstruction, promoting actin stress fiber formation or actin  
CC polymerisation, increasing F:G actin ratio in a smooth muscle cell,  
CC treating or preventing obstructive vascular disease (e.g. restenosis), or  
CC preventing stenosis. The agent that promotes elastin signaling in smooth  
CC muscle cells is useful for decreasing or preventing occlusion of a body  
CC vessel by smooth muscle cells, decreasing vascular obstruction, promoting  
CC actin stress fiber formation or actin polymerization, increasing F:G  
CC actin ratio in a smooth muscle cell, treating or preventing obstructive  
CC vascular disease (e.g. restenosis following angioplasty), or preventing  
CC stenosis. It is also useful in manufacturing a medicament for the  
CC treatment or prevention of occlusion of a vessel. The present sequence is  
CC the human tropoelastin protein as shown in the exemplification of the  
CC invention  
XX Sequence 757 AA;  
SQ Query Match 100.0%; Score 253; DB 7; Length 757;  
Best Local Similarity 100.0%; Pred. No. 6.7e-17; Indels 0; Gaps 0;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGAGIGPLGVGVGPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 49  
|||||  
DB 542 AAAGLGAGIGPLGVGVGPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 590  
|||||  
RESULT 10  
ADP65160  
ID ADP65160 standard; protein; 757 AA.  
XX ADP65160;  
XX 12-AUG-2004 (first entry)  
DT Human elastin.  
DE autoimmune disease; arthritide; gene expression analysis;  
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;  
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;  
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;  
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
KW immune; human.  
XX Homo sapiens.  
OS WO2003072827-A1.  
PN 04-SEP-2003.  
PD 31-OCT-2002; 2002WO-US035433.  
PF 31-OCT-2001; 2001US-0336220P.  
PR (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX Hirsch R, Thorton SL;  
PI WPI; 2003-712740/67.  
XX GENBANK; NP\_000492.  
XX Diagnosing and analyzing autoimmune disease using gene expression  
PT profiles and microarray technology, useful for diagnosing and treating  
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
PT gout.  
XX Disclosure; Page; 56pp; English.

XX The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents a human  
 CC tropoelastin derivative SHEL26-36 excluding exon 26A product  
 XX  
 SQ Sequence 183 AA;

Query Match 83.8%; Score 212; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVGAGVPGFGA 41  
 Db 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41

## RESULT 12

AAAY69138  
 ID AAY69138 standard; protein; 183 AA.

XX  
 AC AAY69138;  
 XX  
 XX  
 DT 30-MAY-2000 (first entry)  
 DE Amino acid sequence of a human tropoelastin derivative.  
 XX  
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX  
 OS Homo sapiens.

XX WO200004043-A1.

XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-AU000580.

XX 17-JUL-1998; 98AU-00004723.

XX (UNSY ) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 2000-182399/16.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.

PS Disclosure; Page 134-135; 136pp; English.

XX The present sequence represents a human tropoelastin derivative, which is  
 CC representative of tropoelastin derivatives of the invention. In the  
 CC tropoelastin derivatives of the invention a subsequence has been mutated  
 CC so that susceptibility to proteolysis is reduced or eliminated, or a  
 CC subsequence has been inserted so that susceptibility to proteolysis is  
 CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary  
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
 CC and for inducing chemotaxis. They are also useful for proliferation or

CC growth inhibition, particularly of smooth muscle cells, epithelial or  
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
 CC derivatives are competitive inhibitors of the protease, and are used for  
 CC protecting against lung damage caused by elastin, for inhibiting or  
 CC controlling localized growth of cancers or metastases, or to limit  
 CC protease activity that causes blood clotting

SQ Sequence 183 AA;

Query Match 83.8%; Score 212; DB 3; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41  
 Db 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41

## RESULT 13

ADB64761  
 ID ADB64761 standard; protein; 617 AA.

XX  
 AC ADB64761;

XX  
 DT 04-DEC-2003 (first entry)

XX Human protein encoded by clone NT2RP70003110.

XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;  
 KW cell regeneration; membrane protein; signal transduction-related protein;  
 KW transcription-related protein; osteoporosis; neurological disease;  
 KW cancer; tumour.

XX Homo sapiens.

XX EP1308459-A2.

XX 07-MAY-2003.

XX 28-MAR-2002; 2002EP-00007401.

XX 05-NOV-2001; 2001JP-00379298.

XX 25-JAN-2002; 2002US-00350978.

XX (HELI-) HELIX RES INST.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;

XX WPI; 2003-450961/43.  
 DR N-PSDB; ADB62791.

XX New polynucleotides and polypeptides, useful for developing a diagnostic  
 PT marker or medicines for regulation of their expression and activity, or  
 PT as targets of gene therapy.

XX Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected  
 CC from 1970 fully defined nucleotide sequences which encode novel  
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
 CC or its partial peptide, an antibody binding to the polypeptide or peptide  
 CC of the polynucleotide, immunologically assaying the polypeptide or  
 CC peptide of the polynucleotide by contacting the polypeptide or peptide  
 CC with the antibody of the encoded protein, and observing the binding  
 CC between the two, a transformant carrying the polynucleotide in an  
 CC expressible manner and an antisense polynucleotide. The oligonucleotide  
 CC is useful as a primer for synthesising the polynucleotide, or as a probe  
 CC for detecting the polynucleotide. The polynucleotides and encoded  
 CC proteins are useful as pharmaceutical agents and many disease-related

CC genes may be included in them, for developing a diagnostic marker or  
 CC medicines for regulation of their expression and activity, or as targets  
 CC of gene therapy. The genes are involved in tissue and/or cell  
 CC regeneration. Membrane proteins, signal transduction-related proteins,  
 CC transcription-related proteins, disease-related proteins and genes  
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate  
 CC the activity or expression of the encoded protein to treat diseases. The  
 CC sequence presented is a protein of the invention. Note: Some of the  
 CC sequence data for this patent is not represented in the printed  
 CC specification, but is based on sequence information supplied by the  
 CC European Patent Office.

XX SQ Sequence 617 AA;  
 Query Match 83.8%; Score 212; DB 7; Length 617;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 41  
 Db 453 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 493

RESULT 14  
 ID AA01303 standard; protein; 660 AA.

XX AC AA01303;  
 XX 07-JUN-1999 (first entry)  
 XX Human tropoelastin derivative SHEldeltamodified.  
 XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KW hand lotion; surgical implant; industrial product; human; SHEL.

XX Homo sapiens.  
 OS Synthetic.  
 XX WO9903886-A1.  
 XX 28-JAN-1999.  
 XX 17-JUL-1998; 98WO-AU000564.  
 XX 18-JUL-1997; 97AU-00008117.  
 XX (UNSY ) UNIV SYDNEY.  
 XX Weiss AS;  
 XX WPI; 1999-132162/11.  
 DR N-PSDB; AAX27705.  
 XX New derivatives of human tropoelastin - with elastin-like or  
 PT macromolecular binding properties, useful e.g. as surgical implants.  
 PS Claim 7; Fig 3; 82pp; English.

XX The invention relates to a derivative or variant of human tropoelastin  
 CC (hTE) having elastin-like and/or macromolecule (specifically  
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
 CC comprising the nucleic acids encoding the variants or derivatives are  
 CC used to produce the proteins recombinantly. The tropoelastin derivatives  
 CC or hybrid proteins containing the derivatives are useful in medical,  
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial  
 CC products. The hybrid protein have controllable GAG-binding properties,  
 CC depending on presence or absence of a specific fragment, designated  
 CC peptide 26A, from hTE. The present sequence represents a human  
 CC tropoelastin derivative SHEldeltamodified

XX SQ Sequence 660 AA;  
 Query Match 83.8%; Score 212; DB 2; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 41  
 Db 479 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 519

RESULT 15  
 ID ADM03792 standard; protein; 663 AA.

XX AC ADM03792;  
 XX 20-MAY-2004 (first entry)  
 XX Human protein of the invention SEQ ID NO:2477.  
 XX human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.  
 XX EPI347046-A1.  
 XX 24-SEP-2003.  
 XX 12-APR-2002; 2002EP-00008400.  
 XX 22-MAR-2002; 2002JP-00137785.  
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehli S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX WPI; 2003-723558/69.  
 DR N-PSDB; ADM01349.  
 XX New polynucleotides and polypeptides are useful in gene therapy, for  
 PT developing a diagnostic marker or medicines for regulating their  
 PT expression and activity, or as a target of gene therapy.  
 XX Claim 1; SEQ ID NO 2477; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded  
 CC polypeptide. A polynucleotide of the invention may have a use in gene  
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
 CC as a primer for synthesizing the polynucleotide or as a probe for  
 CC detecting the polynucleotide. The polynucleotides ADM03758 are  
 CC useful in gene therapy, for developing a diagnostic marker or medicines  
 CC for regulating their expression and activity, or as a target of gene  
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
 CC are useful as pharmaceutical agents. The present sequence represents a  
 CC protein sequence of the invention.

XX SQ Sequence 663 AA;  
 Query Match 83.8%; Score 212; DB 7; Length 663;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 41  
 Db 481 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 521

RESULT 16  
 ADE40134

AD40134 standard; protein; 692 AA.  
ADE40134;  
29-JAN-2004 (first entry)  
Human NOV16b protein - SEQ ID 40.  
NOVX; cardiac; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
anti-diabetic; immunosuppressive; anti-HIV; neuroprotective; norectic;  
antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;  
atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
tissue typing; human; NOV.  
Homo sapiens.  
WO2003064589-A2.  
07-AUG-2003.  
02-AUG-2002; 2002WO-US024483.  
02-AUG-2001; 2001US-0309501P.  
03-AUG-2001; 2001US-0310291P.  
07-AUG-2001; 2001US-0310544P.  
08-AUG-2001; 2001US-0310951P.  
09-AUG-2001; 2001US-0311292P.  
13-AUG-2001; 2001US-0311379P.  
16-AUG-2001; 2001US-0312892P.  
17-AUG-2001; 2001US-0313201P.  
17-AUG-2001; 2001US-0313415P.  
20-AUG-2001; 2001US-0313643P.  
20-AUG-2001; 2001US-0313702P.  
21-AUG-2001; 2001US-0314031P.  
23-AUG-2001; 2001US-0314466P.  
28-AUG-2001; 2001US-0315403P.  
29-AUG-2001; 2001US-0315853P.  
17-SEP-2001; 2001US-0322716P.  
21-SEP-2001; 2001US-0323994P.  
14-DEC-2001; 2001US-0340233P.  
05-FEB-2002; 2002US-0354591P.  
19-MAR-2002; 2002US-0365478P.  
19-APR-2002; 2002US-0373814P.  
19-APR-2002; 2002US-0373825P.  
19-APR-2002; 2002US-0373989P.  
23-APR-2002; 2002US-0374632P.  
07-JUN-2002; 2002US-0386971P.  
01-AUG-2002; 2002US-00210172.  
(CURA-) CURAGEN CORP.  
Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;  
Shimketa RA, Zerhusen BD, Li L, Ji W, Padigar M, Casman SU;  
Voss EE, Boldog FL, Gorman L, Leite MW, Vernet CM, Anderson DW;  
Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;  
Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;  
Alsbrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;  
Smithson G;  
WPI; 2003-663472/62.  
N-PSDB; ADE40133.  
New NOVX polypeptides and nucleic acids, useful for preventing or  
treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
pharmacogenomics.  
Claim 1; SEQ ID NO 40; 560pp; English.  
The invention relates to a novel NOVX polypeptide. The polypeptide of the  
invention demonstrates cardiac, antiarteriosclerotic, hypotensive,

cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
neuroprotective, norectic, antiparkinsonian, antiasthmatic and  
gynaecological activities and may be useful in diagnosing, treating or  
preventing NOVX-associated disorders including cardiomyopathy,  
atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple  
sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
disease, asthma or fertility disorders. Furthermore, the polypeptides may  
be utilised as vaccines whilst the nucleic acids may be used as  
hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
preventive medicine and pharmacogenomics. The current sequence is that of  
the human NOV protein of the invention.  
XX Sequence 692 AA;  
SQ  
Query Match 83.8%; Score 212; DB 7; Length 692;  
Best Local Similarity 100.0%; Pred. No. 6.5e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAAGLGAGTGLGVGVGPGLVGAGVPGLVGAGVPGFCA 41  
|||||  
Db 510 AAAGLGAGTGLGVGVGPGLVGAGVPGLVGAGVPGFCA 550  
RESULT 17  
AA01302  
ID AA01302 standard; protein; 698 AA.  
XX  
AC AA01302;  
XX  
DT 07-JUN-1999 (first entry)  
XX  
DE Human tropoelastin variant SHELDelta26A.  
XX  
KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
hand lotion; surgical implant; industrial product; human; SHEL; variant.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO9903886-A1.  
XX  
PD 28-JAN-1999.  
XX  
PF 17-JUL-1998; 98WO-AU000564.  
XX  
PR 18-JUL-1997; 97AU-00008117.  
XX  
PA (UNSY) UNIV SYDNEY.  
XX  
PI Weiss AS;  
XX  
WPI; 1999-132162/11.  
XX  
PT New derivatives of human tropoelastin - with elastin-like or  
macromolecular binding properties, useful e.g. as surgical implants.  
XX  
PS Claim 13; Fig 2; 82pp; English.  
XX  
CC The invention relates to a derivative or variant of human tropoelastin  
(hTE) having elastin-like and/or macromolecule (specifically  
glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
comprising the nucleic acids encoding the variants or derivatives are  
used to produce the proteins recombinantly. The tropoelastin derivatives  
or hybrid proteins containing the derivatives are useful in medical,  
pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
wrinkle or hand lotions, also as surgical implants, foods and industrial  
products. The hybrid protein have controllable GAG-binding properties,  
depending on presence or absence of a specific fragment, designated  
peptide 26A, from hTE. The present sequence represents the synthetic  
human tropoelastin variant SHELDelta26A  
XX Sequence 698 AA;  
SQ

Mon Nov 22 12:42:43 2004

us-09-743-818a-72.rag

Query Match 83.8%; Score 212; DB 2; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 41  
 DB 516 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 556

RESULT 18  
 AAY69069  
 ID AAY69069 standard; protein; 698 AA.  
 XX  
 AC AAY69069;  
 XX  
 DT 30-MAY-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human reduced tropoelastin derivative.  
 XX  
 KW Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease;  
 KW antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;  
 KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;  
 KW metastasis; blood clotting.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FN WO200004043-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 19-JUL-1999; 99WO-AU000580.  
 XX  
 PR 17-JUL-1998; 98AU-00004723.  
 XX  
 PA (UNSY) UNIV SYDNEY.  
 XX  
 PI Weiss AS;  
 XX  
 DR WPI; 2000-182399/16.  
 DR N-PSDB; AAZ61144.  
 XX  
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.  
 XX  
 PS Disclosure; Page 110-112; 136pp; English.  
 XX  
 CC The present sequence represents a human reduced tropoelastin derivative, designated SHEL-delta-26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting  
 XX  
 SQ Sequence 698 AA;  
 Query Match 83.8%; Score 212; DB 3; Length 698;

Best Local Similarity 100.0%; Pred. No. 6.6e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 41  
 DB 516 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 556  
 RESULT 19  
 ADE40132  
 ID ADE40132 standard; protein; 711 AA.  
 XX  
 AC ADE40132;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOV16a protein - SEQ ID 38.  
 XX  
 KW NOVX; cardiac; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
 KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
 KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;  
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
 KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
 KW tissue typing; human; NOV.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003064589-A2.  
 XX  
 PD 07-AUG-2003.  
 XX  
 PF 02-AUG-2002; 2002WO-US024483.  
 XX  
 PR 02-AUG-2001; 2001US-0309501P.  
 PR 03-AUG-2001; 2001US-0310291P.  
 PR 07-AUG-2001; 2001US-0310544P.  
 PR 08-AUG-2001; 2001US-0310951P.  
 PR 09-AUG-2001; 2001US-0311292P.  
 PR 13-AUG-2001; 2001US-0311979P.  
 PR 16-AUG-2001; 2001US-0312892P.  
 PR 17-AUG-2001; 2001US-0313201P.  
 PR 17-AUG-2001; 2001US-0313415P.  
 PR 20-AUG-2001; 2001US-0313702P.  
 PR 20-AUG-2001; 2001US-0314031P.  
 PR 23-AUG-2001; 2001US-0314466P.  
 PR 28-AUG-2001; 2001US-0315403P.  
 PR 29-AUG-2001; 2001US-0315853P.  
 PR 17-SEP-2001; 2001US-0322716P.  
 PR 21-SEP-2001; 2001US-0323994P.  
 PR 14-DEC-2001; 2001US-0340233P.  
 PR 05-FEB-2002; 2002US-0354591P.  
 PR 19-MAR-2002; 2002US-0365478P.  
 PR 19-APR-2002; 2002US-0373814P.  
 PR 19-APR-2002; 2002US-0373825P.  
 PR 19-APR-2002; 2002US-0373989P.  
 PR 23-APR-2002; 2002US-0374632P.  
 PR 07-JUN-2002; 2002US-0386971P.  
 PR 01-AUG-2002; 2002US-00210172.  
 XX  
 CC (CURA-) CURAGEN CORP.  
 XX  
 PA Keskula R, Miller CE, Patturajan M, Pena CEA, Rieger DK;  
 PI Shimketa RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;  
 PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;  
 PI Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;  
 PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;  
 PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;  
 PI Smithson G;  
 XX  
 DR WPI; 2003-663472/62.  
 DR N-PSDB; ADE40131.

XX New NOVX polypeptides and nucleic acids, useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, or  
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX  
 PS Claim 1; SEQ ID NO 38; 560pp; English.  
 XX  
 CC The invention relates to a novel NOVX polypeptide. The polypeptide of the  
 CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,  
 CC cytotatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
 CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and  
 CC gynaecological activities and may be useful in diagnosing, treating or  
 CC preventing NOVX-associated disorders including cardiomyopathy,  
 CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple  
 CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
 CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
 CC be utilised as vaccines whilst the nucleic acids may be used as  
 CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
 CC preventive medicine and pharmacogenomics. The current sequence is that of  
 CC the human NOV protein of the invention.  
 XX  
 SQ Sequence 711 AA;

Query Match 83.8%; Score 212; DB 7; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGTGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 41  
 DB 547 AAAGLGAGTGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 587

RESULT 20  
 AAB08630  
 ID AAB08630 standard; peptide; 712 AA.  
 AC AAB08630;  
 XX  
 XX 20-DEC-2000 (first entry)  
 DE Amino acid sequence of a human elastin polypeptide.  
 XX  
 KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;  
 KW smooth muscle cell differentiation; smooth muscle cell migration;  
 KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;  
 KW vascular bypass graft stenosis; transplant arteriopathy; dissection;  
 KW SVAS; hypertension; transplant arteriopathy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200050068-A2.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 28-FEB-2000; 2000WO-US002526.  
 XX  
 PR 26-FEB-1999; 99US-00258217.  
 XX  
 PA (UTAH ) UNIV UTAH RES FOUND.  
 XX  
 PI Keating MT, Li DY;  
 XX  
 DR WPI; 2000-533134/48.  
 XX  
 PT Elastin based compositions useful for treating atherosclerosis,  
 PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,  
 PT aneurysm, dissection SVAS and/or hypertension.  
 XX  
 PS Example 3; Page 46; 79pp; English.  
 XX  
 CC The present sequence represents a human elastin. Peptides derived from  
 CC elastin are used in compositions of the invention. The specification

CC describes elastin based compositions that are potent regulators of smooth  
 CC muscle cell proliferation, differentiation and migration in vivo. The  
 CC elastin-based compositions comprise at least one elastic fibre, elastins,  
 CC tropoelastins (or fragments of them) which have biological activities  
 CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;  
 CC stimulating the differentiation of smooth muscle cells in vivo; and  
 CC regulating the migration of smooth muscle cells in vivo. The compositions  
 CC may be used for the prophylaxis or treatment of a disorder characterized  
 CC by diminished capacity to regulate smooth muscle cell function such as  
 CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant  
 CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated  
 CC also include SVAS (undefined), hypertension, and transplant arteriopathy  
 XX

SQ Sequence 712 AA;

Query Match 83.8%; Score 212; DB 3; Length 712;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGTGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 41  
 DB 548 AAAGLGAGTGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 588

RESULT 21  
 AAB08631  
 ID AAB08631 standard; peptide; 730 AA.  
 AC AAB08631;  
 XX  
 XX 20-DEC-2000 (first entry)  
 DE Fusion protein comprising human elastin and c-myc.  
 XX  
 KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;  
 KW smooth muscle cell differentiation; smooth muscle cell migration;  
 KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;  
 KW vascular bypass graft stenosis; transplant arteriopathy; dissection;  
 KW SVAS; hypertension; transplant arteriopathy.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS Unidentified.  
 XX  
 PN WO200050068-A2.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 28-FEB-2000; 2000WO-US002526.  
 XX  
 PR 26-FEB-1999; 99US-00258217.  
 XX  
 PA (UTAH ) UNIV UTAH RES FOUND.  
 XX  
 PI Keating MT, Li DY;  
 XX  
 DR WPI; 2000-533134/48.  
 XX  
 PT Elastin based compositions useful for treating atherosclerosis,  
 PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,  
 PT aneurysm, dissection SVAS and/or hypertension.  
 XX  
 PS Example 3; Page 48; 79pp; English.  
 XX  
 CC The present sequence represents a fusion protein, comprising human  
 CC elastin and c-myc, preceded by a His tag. The protein is used in  
 CC compositions of the invention. The specification describes elastin based  
 CC compositions that are potent regulators of smooth muscle cell  
 CC proliferation, differentiation and migration in vivo. The elastin-based  
 CC compositions comprise at least one elastic fibre, elastins, tropoelastins  
 CC (or fragments of them) which have biological activities comprising:  
 CC inhibiting the proliferation of smooth muscle cells in vivo; stimulating  
 CC the differentiation of smooth muscle cell in vivo; and regulating the

CC migration of smooth muscle cells in vivo. The compositions may be used  
CC for the prophylaxis or treatment of a disorder characterized by  
CC diminished capacity to regulate smooth muscle cell function such as  
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant  
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated  
CC also include SVAS (undefined), hypertension, and transplant arteriopathy  
XX  
SQ Sequence 730 AA;

Query Match 83.8%; Score 212; DB 3; Length 730;  
Best Local Similarity 100.0%; Pred. No. 6.9e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLVGAGVPGFGA 41  
DB 557 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLVGAGVPGFGA 597

RESULT 22  
AAO17360  
ID AAO17360 standard; protein; 730 AA.

XX AAO17360;  
DT 19-JUL-2002 (first entry)  
DE Human elastin.

XX Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;  
KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;  
KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;  
KW transmembrane receptor PTK7; collagen type XVIII alpha 1;  
KW platelet derived growth factor receptor alpha; laminin M chain;  
KW subtilisin like protein PACE4; nidogen.

XX Homo sapiens.

OS

XX EPI191107-A2.

XX 27-MAR-2002.

XX 21-AUG-2001; 2001EP-00250300.

XX 25-SEP-2000; 2000DE-01048633.

XX (SCHD ) SCHERING AG.

XX Hess-Stumpp H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;

XX Regidor P, Scotti S;

XX WPI; 2002-317413/36.

XX In vitro diagnosis and monitoring of endometriosis, comprises detecting  
PT reduced expression of specific gene products, e.g. from the fibronectin  
PT gene.

XX Claim 1; Page 15-16; 21pp; German.

XX The present invention relates to a method for the in vitro diagnosis of  
CC endometriosis by determining the amount of gene product from at least one  
CC specific gene in a patient sample and comparing this with the amount of  
CC gene product in a control sample. A reduced level is indicative of  
CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,  
CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,  
CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,  
CC transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet  
CC derived growth factor receptor alpha, laminin M chain, subtilisin like  
CC protein PACE4 or nidogen. The method is useful for initial diagnosis of  
CC endometriosis, and also for monitoring progress and treatment of the  
CC disease. The present sequence is human elastin

XX Sequence 730 AA;

Query Match 83.8%; Score 212; DB 5; Length 730;  
Best Local Similarity 100.0%; Pred. No. 6.9e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLVGAGVPGFGA 41  
DB 548 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLVGAGVPGFGA 588

RESULT 23  
ADQ19747  
ID ADQ19747 standard; protein; 730 AA.

XX ADQ19747;  
DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.

XX Example 2; SEQ ID NO 2566; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytostatic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC protein of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 730 AA;

Query Match 83.8%; Score 212; DB 8; Length 730;  
Best Local Similarity 100.0%; Pred. No. 6.9e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLVGAGVPGFGA 41  
DB 548 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLVGAGVPGFGA 588

RESULT 24  
ADE08527  
ID ADE08527 standard; protein; 870 AA.

XX



AC ADE08527;  
 DT 29-JAN-2004 (first entry)  
 DE Novel protein (useful for identifying genetic disorders) #682.  
 DE novel gene; novel protein; tissue marker; molecular weight marker;  
 KW chromosome marker; genetic disorder.  
 XX Unidentified.  
 OS  
 XX WO2003054152-A2.  
 PN 03-JUL-2003.  
 PD  
 PD 10-DEC-2002; 2002WO-US039555.  
 PF  
 PF 10-DEC-2001; 2001US-0339739P.  
 PR 11-DEC-2001; 2001US-0339453P.  
 PR 14-MAR-2002; 2002US-0365091P.  
 PR 14-MAR-2002; 2002US-0365384P.  
 PR 12-APR-2002; 2002US-0372381P.  
 PR 12-APR-2002; 2002US-0372615P.  
 PR 22-APR-2002; 2002US-00128558.  
 PR 24-APR-2002; 2002US-0376045P.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
 XX WPI; 2003-569235/53.  
 DR N-PSDB; ADE07616.  
 DR  
 DR  
 XX New polynucleotides, useful for expressing recombinant proteins for  
 PT analysis, characterization or therapeutic use, or as markers for tissues  
 PT in which the corresponding protein is preferentially expressed.  
 XX  
 XX Claim 20; SEQ ID NO 1593; 1177pp; English.  
 PS  
 CC The invention comprises the amino acid and coding sequences of novel  
 CC proteins. The DNA and protein sequences of the invention are useful as:  
 CC markers for tissues in which the corresponding protein is preferentially  
 CC expressed; as molecular weight markers on gels; as chromosome markers or  
 CC tags; to identify chromosomes or to map related gene positions; and to  
 CC compare with endogenous DNA sequences in patients to identify potential  
 CC genetic disorders. The present amino acid sequence represents a protein  
 CC of the invention.  
 XX  
 SQ Sequence 870 AA;  
 Query Match 83.8%; Score 212; DB 7; Length 870;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-13;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGLGVGAGVPGFGA 41  
 DB 613 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGLGVGAGVPGFGA 653  
 RESULT 25  
 AAB88422  
 ID AAB88422 standard; protein; 472 AA.  
 XX  
 XX AAB88422;  
 AC  
 XX  
 DT 23-MAY-2001 (first entry)  
 DE Human membrane or secretory protein clone PSEC0191.  
 DE Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes.

XX Homo sapiens.  
 OS  
 XX EPI067182-A2.  
 PN  
 XX 10-JAN-2001.  
 PD  
 PD 07-JUL-2000; 2000EP-00114090.  
 PF  
 PF 08-JUL-1999; 99JP-00194179.  
 PR 11-JAN-2000; 2000JP-00118775.  
 PR 02-MAY-2000; 2000JP-00183766.  
 XX  
 XX (HELI-) HELIX RES INST.  
 PA  
 XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 PI WPI; 2001-093989/11.  
 DR N-PSDB; AAF93849.  
 DR  
 XX Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development.  
 PT  
 XX Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.  
 PS  
 XX  
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAB88317  
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene  
 CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbant assay (ELISA). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes  
 XX  
 SQ Sequence 472 AA;  
 Query Match 82.2%; Score 208; DB 4; Length 472;  
 Best Local Similarity 97.6%; Pred. No. 1.1e-12;  
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGLGVGAGVPGFGA 41  
 DB 316 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGLGVGAGVPGFGA 356  
 RESULT 26  
 AAY69071  
 ID AAY69071 standard; protein; 571 AA.  
 XX  
 XX AAY69071;  
 AC  
 XX  
 DT 30-MAY-2000 (first entry)  
 DE Amino acid sequence of a human tropoelastin derivative.  
 DE Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 XX hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

OS Homo sapiens.  
XX WO200004043-A1.  
XX 27-JAN-2000.  
XX 19-JUL-1999; 99WO-AU000580.  
XX 17-JUL-1998; 98AU-00004723.  
XX (UNSY ) UNIV SYDNEY.  
XX Weiss AS;  
XX WPI; 2000-182399/16.  
XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.  
XX Disclosure; Page 115-117; 136pp; English.  
XX The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting  
XX Sequence 571 AA;  
SQ Query Match 74.7%; Score 189; DB 3; Length 571;  
Best Local Similarity 94.9%; Pred. No. 1e-10;  
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AAAGLGAGIPGLGVGVGVPLGLGVGAGVPLGLGVGAGVPGF 39  
DB 516 AAAGLGAGIPGLGVGVGVPLGLGVGAGVPLGLGVGAGVPGF 554  
RESULT 27  
ADE56670  
ID ADE56670 standard; protein; 864 AA.  
XX ADE56670;  
XX 29-JAN-2004 (first entry)  
XX Rat Protein Q99372, SEQ ID NO 2524.  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX Rattus norvegicus.  
XX WO2003016475-A2.  
XX 27-FEB-2003.  
XX

PF 14-AUG-2002; 2002WO-US025765.  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
DR GENBANK; Q99372.  
XX New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.  
XX Claim 1; Page; 1017pp; English.  
XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)). In an animal (shown in Table 2 of therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 864 AA;  
SQ Query Match 71.5%; Score 181; DB 7; Length 864;  
Best Local Similarity 78.3%; Pred. No. 9e-10;  
Matches 36; Conservative 1; Mismatches 7; Indels 2; Gaps 1;  
QY 1 AAAGLGAGIPGLGVGVGVPLGLGVGAGVPLGLGVGAGVPGF 46  
DB 622 AAAGLGAGVPLGLGVGVGVPLGLGVGAGVPLGLGVGAGVPGF 665  
RESULT 28  
AAP71455  
ID AAP71455 standard; peptide; 34 AA.  
XX AAP71455;  
XX 25-MAR-2003 (revised)  
DT 09-JAN-2003 (revised)  
DT 13-JUN-1991 (first entry)  
XX Sequence of chemotactic peptides which is incorporated into the surface of a prosthetic device.  
XX Fibroblast; elastic fibres; tissue regeneration; skin tissue;  
XX blood vessel walls.  
XX





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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 105.249 Seconds  
(without alignments)  
1755.321 Million cell updates/sec

Title: US-09-743-818a-71

Perfect score: 2680

Sequence: 1 GGVDGALPGGVGVFGVPGA.....GGVAAAKSAKVAQAQLR 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A\_genseq23Sep04.\*  
2: genseq23Sep04.\*  
3: genseq23Sep04.\*  
4: genseq23Sep04.\*  
5: genseq23Sep04.\*  
6: genseq23Sep04.\*  
7: genseq23Sep04.\*  
8: genseq23Sep04.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2680	100.0	515	3	AAY69135 Amino aci
2	2680	100.0	571	3	AAY69071 Amino aci
3	2680	100.0	698	2	AAY01302 Human tro
4	2680	100.0	698	3	AAY69069 Amino aci
5	2680	100.0	730	2	AAW46315 Human ela
6	2680	100.0	731	3	AAY69068 Human ela
7	2680	100.0	731	4	AAY69068 Human ela
8	2680	100.0	733	2	AAK56657 Human ela
9	2680	100.0	733	2	AAK56653 Synthetic
10	2680	100.0	757	2	AAY01301 Amino aci
11	2680	100.0	757	7	ABG75223 Human tro
12	2672	99.7	731	7	ADP65160 Human ela
13	2670	99.6	731	6	ADP65160 Human ela
14	2667.5	99.5	711	7	ABU08725 Human ela
15	2667	99.5	730	5	AAO17360 Human ela
16	2667	99.5	730	8	AAO17360 Human ela
17	2663	99.4	712	3	AAO17360 Human ela
18	2663	99.4	730	3	AAO17360 Human ela
19	2431	90.7	692	7	ADP65160 Human ela
20	2353	87.8	870	7	ADP65160 Human ela
21	2328	86.9	660	2	ADP65160 Human ela
22	2306.5	86.1	663	7	ADP65160 Human ela
23	2129.5	79.5	617	7	ADP65160 Human ela
24	1675.5	62.5	864	7	ADP65160 Human ela
25	1314	49.0	472	4	AAH88422 Human mem

26	911.5	34.0	745	2	AAY31682	Aay31682 Alanine-c
27	890	33.2	988	2	AAR80253	Aar80253 Polymer S
28	890	33.2	988	5	ABP53474	Abp53474 Protein p
29	872	32.5	832	2	AAR80252	Aar80252 Polymer S
30	872	32.5	832	5	ABP53473	Abp53473 Protein p
31	870	32.5	936	2	AAR80251	Aar80251 Polymer S
32	870	32.5	936	5	ABP53472	Abp53472 Protein p
33	864	32.2	1056	2	AAR80254	Aar80254 Polymer S
34	864	32.2	1056	5	ABP53475	Abp53475 Protein p
35	850	31.7	972	2	AAR80255	Aar80255 Polymer S
36	850	31.7	972	5	ABP53476	Abp53476 Protein p
37	849.5	31.7	1412	2	AAW53519	Aaw53519 Amino aci
38	849.5	31.7	1413	1	AAW53519	Aaw53519 Amino aci
39	849.5	31.7	1413	1	AAW53519	Aaw53519 Amino aci
40	849.5	31.7	1413	2	AAW53519	Aaw53519 Amino aci
41	849.5	31.7	1464	3	AAW78278	Aaw78278 EBSI synt
42	849.5	31.7	1465	5	ABG69268	Abg69268 Elastin-l
43	849.5	31.7	1465	7	ABG69268	Abg69268 Elastin-l
44	848.5	31.7	1002	2	AAW09218	Aaw09218 Recombina
45	848.5	31.7	1002	2	AAW09218	Aaw09218 Recombina
46	848.5	31.7	1002	3	AAW53544	Aaw53544 Amino aci
47	848.5	31.7	1002	5	ABG31418	Abg31418 SELPK pr
48	848.5	31.7	1002	7	ABW01634	Abw01634 Plasmid p
49	847	31.6	1040	5	ABP53478	Abp53478 Protein p
50	846.5	31.6	696	8	ADK51953	Adk51953 Repeat pr
51	844.5	31.5	968	5	AAE18320	Aae18320 Silk elas
52	844.5	31.5	2257	1	AAW82961	Aaw82961 SELPK3 pro
53	844.5	31.5	2257	2	AAW82961	Aaw82961 SELPK3 pro
54	844.5	31.5	2257	2	AAW82961	Aaw82961 SELPK3 pro
55	844.5	31.5	2257	2	AAW82961	Aaw82961 SELPK3 pro
56	844.5	31.5	2257	3	AAW82961	Aaw82961 SELPK3 pro
57	844.5	31.5	2257	5	ABG69272	Abg69272 Silk/Elas
58	844.5	31.5	696	8	ADK51955	Adk51955 Repeat pr
59	843.5	31.5	696	8	ADK51955	Adk51955 Repeat pr
60	842.5	31.4	696	5	ABP53470	Abp53470 SELPK re
61	842.5	31.4	696	5	ABP53482	Abp53482 Protein p
62	842.5	31.4	768	5	ABP53466	Abp53466 SELPK8 rel
63	842.5	31.4	877	2	AAW80335	Aaw80335 Protein p
64	842.5	31.4	877	2	AAW80335	Aaw80335 Protein p
65	841.5	31.4	936	2	AAW09221	Aaw09221 SELPK-CS
66	841.5	31.4	936	3	AAW51891	Aaw51891 Plasmid p
67	841.5	31.4	936	5	ABG31421	Abg31421 SELPK-CS
68	841.5	31.4	937	2	ABW01637	Abw01637 Plasmid p
69	841.5	31.4	937	2	ABW01637	Abw01637 Plasmid p
70	837	31.2	768	5	ABP53481	Abp53481 Protein p
71	837	31.2	884	2	AAW09213	Aaw09213 SELPK po
72	837	31.2	884	2	AAW09213	Aaw09213 SELPK po
73	837	31.2	884	2	AAW53541	Aaw53541 Expected
74	837	31.2	884	2	AAW53541	Aaw53541 Expected
75	837	31.2	884	3	AAW51882	Aaw51882 Plasmid p
76	837	31.2	884	5	ABG31412	Abg31412 SELPK po
77	837	31.2	884	7	ABW01628	Abw01628 Plasmid p
78	834.5	31.1	1024	5	ABP53477	Abp53477 Protein p
79	834.5	31.1	1024	5	ABP53477	Abp53477 Protein p
80	829	30.9	768	5	ABP53461	Abp53461 SELPK rel
81	822.5	30.7	2055	1	AAW82960	Aaw82960 SELPK2 pro
82	822.5	30.7	2055	2	AAW82960	Aaw82960 SELPK2 pro
83	822.5	30.7	2055	2	AAW82960	Aaw82960 SELPK2 pro
84	822.5	30.7	2055	2	AAW82960	Aaw82960 SELPK2 pro
85	822.5	30.7	2055	3	AAW82960	Aaw82960 SELPK2 pro
86	822.5	30.7	2055	5	ABG69271	Abg69271 Silk/Elas
87	822.5	30.7	2055	5	ABG69271	Abg69271 Silk/Elas
88	804.5	30.0	780	8	ADK51951	Adk51951 Repeat pr
89	793	29.6	966	3	AAW51893	Aaw51893 SELPK-CS
90	793	29.6	966	3	AAW51893	Aaw51893 SELPK-CS
91	793	29.6	966	3	AAW51893	Aaw51893 SELPK-CS
92	793	29.6	966	7	ABW01639	Abw01639 Plasmid p
93	784.5	29.3	450	5	AAU77399	Aau77399 Elastin-l
94	778.5	29.0	1085	2	AAW50046	Aaw50046 N. clavip
95	777.5	29.0	777	5	AAW50046	Aaw50046 N. clavip
96	777.5	29.0	777	5	AAW50046	Aaw50046 N. clavip
97	774.5	28.9	975	5	ABW05207	Abw05207 Elastin m
98	774	28.9	782	2	AAW31680	Aaw31680 Fibronect

Mon Nov 22 12:42:42 2004

99 774 28.9 2003 2 AAY31695 Aay31695 Fibrinect  
100 766 28.6 600 3 AAY80346 Aay80346 Synthetic

ALIGNMENTS

RESULT 1

AA69135 standard; protein; 515 AA.

XX AC AAY69135;  
XX DT 30-MAY-2000 (first entry)  
XX DE Amino acid sequence of a human tropoelastin derivative.  
XX KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
XX KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
XX KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
XX OS Homo sapiens.

XX WO200004043-A1.

XX PD 27-JAN-2000.

XX PF 19-JUL-1999; 99WO-AU000580.

XX PR 17-JUL-1998; 98AU-00004723.

XX PA (UNSY ) UNIV SYDNEY.

XX PI Weiss AS;

XX DR WPI; 2000-182399/16.

XX PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
XX PT cell growth.

XX PS Disclosure; Page 131-133; 136pp; English.

XX CC The present sequence represents a human tropoelastin derivative, which is  
XX CC representative of tropoelastin derivatives of the invention. In the  
XX CC tropoelastin derivatives of the invention a subsequence has been mutated  
XX CC so that susceptibility to proteolysis is reduced or eliminated, or a  
XX CC subsequence has been inserted so that susceptibility to proteolysis is  
XX CC increased. The derivatives have with reduced susceptibility, and can be  
XX CC used where the wild-type protein would be degraded too easily, e.g. in  
XX CC contact with serum or wound exudate. The tropoelastin derivatives provide  
XX CC competitive inhibition of protease activity. The tropoelastin  
XX CC derivatives, and other polypeptides containing tropoelastin derivative-  
XX CC derived protease-susceptibility sites, are useful in human or veterinary  
XX CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents  
XX CC and for inducing chemotaxis. They are also useful for proliferation or  
XX CC growth inhibition, particularly of smooth muscle cells, epithelial or  
XX CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
XX CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
XX CC derivatives are competitive inhibitors of the protease, and are used for  
XX CC protecting against lung damage caused by elastin, for inhibiting or  
XX CC controlling localized growth of cancers or metastases, or to limit  
XX CC protease activity that causes blood clotting

XX SQ Sequence 515 AA;

Query Match 100.0%; Score 2680; DB 3; Length 515;

Best local Similarity 100.0%; Pred. No. 5.4e-153;

Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPFALPGGVPGGVFFPGALGGALGPGGKPLKPVPGGLAGLGLGALGAFPAVT 60

DB 1 GGVPFALPGGVPGGVFFPGALGGALGPGGKPLKPVPGGLAGLGLGALGAFPAVT 60

QY 61 FPGALVPGGVADAAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPOPGAGVKPKVPGVGL 120  
DB |||||  
QY 61 FPGALVPGGVADAAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPOPGAGVKPKVPGVGL 120  
DB |||||  
QY 121 PGVYPGVILPGARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFPGVPGVPLGY 180  
DB |||||  
QY 121 PGVYPGVILPGARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFPGVPGVPLGY 180  
DB |||||  
QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAAGKAGYPTGTGTGVPQAAAAAKAAAF 240  
DB |||||  
QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAAGKAGYPTGTGTGVPQAAAAAKAAAF 240  
DB |||||  
QY 241 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVTPAAAAAATAAATAAAGLVPGG 300  
DB |||||  
QY 241 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVTPAAAAAATAAATAAAGLVPGG 300  
DB |||||  
QY 301 PGFGPVVPGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPAAAAKAAKAYGAR 360  
DB |||||  
QY 301 PGFGPVVPGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPAAAAKAAKAYGAR 360  
DB |||||  
QY 361 PGVGVGGIPTYGVGAGGPGFGVGVGGIPGVAGVPSVGGVPGVPGVGI SPSAQAAAA 420  
DB |||||  
QY 361 PGVGVGGIPTYGVGAGGPGFGVGVGGIPGVAGVPSVGGVPGVPGVGI SPSAQAAAA 420  
DB |||||  
QY 421 AKAAKYGVGTTPAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 480  
DB |||||  
QY 421 AKAAKYGVGTTPAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 480  
DB |||||  
QY 481 VGVAPGVGVAPGIPGGVAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 515  
DB |||||  
QY 481 VGVAPGVGVAPGIPGGVAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 515  
DB |||||

RESULT 2

AA69071 standard; protein; 571 AA.

XX AC AAY69071;

XX DT 30-MAY-2000 (first entry)

XX DE Amino acid sequence of a human tropoelastin derivative.

XX KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
XX KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
XX KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

XX OS Homo sapiens.

XX WO200004043-A1.

XX PD 27-JAN-2000.

XX PF 19-JUL-1999; 99WO-AU000580.

XX PR 17-JUL-1998; 98AU-00004723.

XX PA (UNSY ) UNIV SYDNEY.

XX PI Weiss AS;

XX DR WPI; 2000-182399/16.

XX PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
XX PT cell growth.

XX PS Disclosure; Page 115-117; 136pp; English.

XX CC The present sequence represents a human tropoelastin derivative, which is  
XX CC representative of tropoelastin derivatives of the invention. In the  
XX CC tropoelastin derivatives of the invention a subsequence has been mutated  
XX CC so that susceptibility to proteolysis is reduced or eliminated, or a  
XX CC subsequence has been inserted so that susceptibility to proteolysis is

CC increased. The derivatives have with reduced susceptibility, and can be  
 CC used where the wild-type protein would be degraded too easily, e.g. in  
 CC contact with serum or wound exudate. The tropoelastin derivatives provide  
 CC competitive inhibition of protease activity. The tropoelastin  
 CC derivatives, and other polypeptides containing tropoelastin derivative-  
 CC derived protease-susceptibility sites, are useful in human or veterinary  
 CC medicine, cosmetics (e.g. anti-wrinkle or hand lotions), as bulking agents  
 CC and for inducing chemotaxis. They are also useful for proliferation or  
 CC growth inhibition, particularly of smooth muscle cells, epithelial or  
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.  
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin  
 CC derivatives are competitive inhibitors of the protease, and are used for  
 CC protecting against lung damage caused by elastin, for inhibiting or  
 CC controlling localized growth of cancers or metastases, or to limit  
 CC protease activity that causes blood clotting  
 XX  
 SQ Sequence 571 AA;

Query Match 100.0%; Score 2680; DB 3; Length 571;  
 Best Local Similarity 100.0%; Pred. No. 6e-153;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGVPGAIPGGVPGGVFYPGAGLGGGALGPGKPLKPVPGGLAGAGLGAFFAVT 60  
 Db |||||  
 QY 1 GGVPGAIPGGVPGGVFYPGAGLGGGALGPGKPLKPVPGGLAGAGLGAFFAVT 60  
 Db |||||  
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVVPPGAGVPGKVPVGL 120  
 Db |||||  
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVVPPGAGVPGKVPVGL 120  
 Db |||||  
 QY 121 PGVYPGGVLPGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 180  
 Db |||||  
 QY 121 PGVYPGGVLPGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 180  
 Db |||||  
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 Db |||||  
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 Db |||||  
 QY 241 GAGAAGVLPFGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 300  
 Db |||||  
 QY 241 GAGAAGVLPFGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 300  
 Db |||||  
 QY 301 PGFGPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360  
 Db |||||  
 QY 301 PGFGPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360  
 Db |||||  
 QY 361 PGVYPGGVLPGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420  
 Db |||||  
 QY 361 PGVYPGGVLPGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420  
 Db |||||  
 QY 421 AKAAYGVGTTPAAAATAKAAKAAQFGLVPGVPGVPGVPGVPGVPGVPGVPGVPGV 480  
 Db |||||  
 QY 421 AKAAYGVGTTPAAAATAKAAKAAQFGLVPGVPGVPGVPGVPGVPGVPGVPGVPGV 480  
 Db |||||  
 QY 481 VGVAPGVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515  
 Db |||||  
 QY 481 VGVAPGVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515  
 Db |||||

RESULT 3  
 ID AAY01302  
 AC AAY01302 standard; protein; 698 AA.  
 XX  
 XX AAY01302;  
 DT 07-JUN-1999 (first entry)  
 XX  
 XX Human tropoelastin variant SHELDelta26A.  
 DE  
 DE Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;  
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;  
 KW hand lotion; surgical implant; industrial product; human; SHEL; variant.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO9903886-A1.  
 XX  
 XX 28-JAN-1999.  
 XX  
 XX 17-JUL-1998; 98WO-AU000564.  
 XX  
 XX 18-JUL-1997; 97AU-00008117.  
 XX  
 XX (UNSY ) UNIV SYDNEY.  
 XX  
 XX Weiss AS;  
 XX  
 XX WPI; 1999-132162/11.  
 XX  
 XX New derivatives of human tropoelastin - with elastin-like or  
 XX macromolecular binding properties, useful e.g. as surgical implants.  
 XX  
 XX Claim 13; Fig 2; 82pp; English.  
 XX  
 XX The invention relates to a derivative or variant of human tropoelastin  
 XX (hTE) having elastin-like and/or macromolecule (specifically  
 XX glycosaminoglycan (GAG))-binding properties. Cells containing vectors  
 XX comprising the nucleic acids encoding the variants or derivatives are  
 XX used to produce the proteins recombinantly. The tropoelastin derivatives  
 XX or hybrid proteins containing the derivatives are useful in medical,  
 XX pharmaceutical, veterinary and cosmetic applications, e.g. as anti-  
 XX wrinkle or hand lotions, also as surgical implants, foods and industrial  
 XX products. The hybrid protein have controllable GAG-binding properties,  
 XX depending on presence or absence of a specific fragment designated  
 XX peptide 26A, from hTE. The present sequence represents the synthetic  
 XX human tropoelastin variant SHELDelta26A  
 XX  
 SQ Sequence 698 AA;

Query Match 100.0%; Score 2680; DB 2; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-153;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGVPGAIPGGVPGGVFYPGAGLGGGALGPGKPLKPVPGGLAGAGLGAFFAVT 60  
 Db |||||  
 QY 1 GGVPGAIPGGVPGGVFYPGAGLGGGALGPGKPLKPVPGGLAGAGLGAFFAVT 60  
 Db |||||  
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVVPPGAGVPGKVPVGL 120  
 Db |||||  
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVVPPGAGVPGKVPVGL 120  
 Db |||||  
 QY 121 PGVYPGGVLPGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 180  
 Db |||||  
 QY 121 PGVYPGGVLPGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 180  
 Db |||||  
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 Db |||||  
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 Db |||||  
 QY 241 GAGAAGVLPFGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 300  
 Db |||||  
 QY 241 GAGAAGVLPFGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 300  
 Db |||||  
 QY 301 PGFGPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360  
 Db |||||  
 QY 301 PGFGPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360  
 Db |||||  
 QY 361 PGVYPGGVLPGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420  
 Db |||||  
 QY 361 PGVYPGGVLPGARPPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420  
 Db |||||  
 QY 421 AKAAYGVGTTPAAAATAKAAKAAQFGLVPGVPGVPGVPGVPGVPGVPGVPGVPGV 480  
 Db |||||  
 QY 421 AKAAYGVGTTPAAAATAKAAKAAQFGLVPGVPGVPGVPGVPGVPGVPGVPGVPGV 480  
 Db |||||

RESULT 5	
AAW46315	
ID	AAW46315 standard; protein; 730 AA.
XX	
AC	AAW46315;
XX	
DT	23-JUL-1998 (first entry)
XX	
DE	Human elastin containing non-natural polypeptide MFU-1 sequence.
XX	
XX	MFU-1; minimal functional unit; elastin; human; fibrous protein;
KW	beta-sheet; coating; wound dressing.
KW	
XX	
XX	
OS	Homo sapiens.
XX	
XX	Key
XX	Location/Qualifiers
PH	374. .499
FT	/note= "MFU-1 polypeptide"
FT	
XX	
XX	W09805685-A2.
XX	
XX	12-FEB-1998.
PD	
XX	
XX	07-AUG-1997; 97WO-CA000560.
PF	
XX	
XX	07-AUG-1996; 96US-0023552P.
PR	
XX	07-AUG-1997; 97US-00911364.
PR	
XX	
XX	(PROT-) PROTEIN SPECIALTIES LTD.
PA	(HOSP-) HOSPITAL FOR SICK CHILDREN.
XX	
XX	Rothstein A, Keeley FW, Rothstein SJ;
PI	
XX	
XX	WPI; 1998-145551/13.
DR	
XX	
XX	New non-natural polypeptide with multiple beta-sheet, beta-turn
PT	structures - particularly based on human elastin, useful for coating
PT	protheses, as wound dressings, etc., allows ingrowth of cells.
PT	

WI: 2000-182399/16.  
 N-PSDB; AAZ61144.  
 New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.  
 Disclosure; Page 110-112; 135pp; English.  
 The present sequence represents a human reduced tropoelastin derivative, designated SHEL-delta-26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting  
 Sequence 698 AA;  
 Query Match 100.0%; Score 2680; DB 3; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-153;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 GGVGGAIPGGVGGVYPGAGLGGALGGGALPGCGKDLKPPGGGAGLGGALGGAPAVT 60



XX Claim 5; Fig 1B; 39pp; English.

XX This represents the human elastin sequence containing the minimal functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is not a naturally occurring fibrous protein. Each beta-sheet structure has 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at least 1 amino acid that can take part in crosslinking. The polypeptide can also be derived from the sequences of animal elastin, lamprin and spider silk protein. The MFU polypeptides are self-aligning peptides having the same primary structure as part of a natural fibrous protein. They are used to coat prostheses made of animal or synthetic material or metal, particularly for use as blood vessel or heart valve replacements, wound or burn dressings, or stents. They can be used in cosmetic, elastic or high-tensile strength materials, e.g. ropes or parachute cord. Prostheses based on the MFU allow penetration of endothelial cells, so become permanent living tissue replacements. The MFU polypeptides have better biocompatibility than known elastin-based materials. They are well defined, homogeneous material and are easier to manipulate and produce than full-length elastins. They are non-thrombogenic and non-immunogenic. Materials can be made from 2 or more different MFU polypeptides to allow properties to be tailored for particular applications, e.g. combining the high extensibility of elastin and the high tensile strength of spider silk protein

XX SQ Sequence 730 AA;

Query Match 100.0%; Score 2680; DB 2; Length 730;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-153;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVPGVPGAGLGGALGGALGGKPLKVPVGGLAGAGLGAFFPAVT 60  
 DB 1 GGVPGAIPGGVPGGVPGVPGAGLGGALGGALGGKPLKVPVGGLAGAGLGAFFPAVT 60

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPPQAGVKPKVPGVGL 120  
 DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPPQAGVKPKVPGVGL 120

QY 121 PGVYPGGVLPGARFFPGVGLPGVPTGAGVKPKAGVGGAGAGVPGVGGVAGVPPQAGVKPKVPGVGL 180  
 DB 121 PGVYPGGVLPGARFFPGVGLPGVPTGAGVKPKAGVGGAGAGVPGVGGVAGVPPQAGVKPKVPGVGL 180

QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGGVAGAGKAGYPTGTGVPQAAAAAAYKAAKAF 240  
 DB 181 PIKAPKLPGGYGLPYTTGKLPYGYGGVAGAGKAGYPTGTGVPQAAAAAAYKAAKAF 240

QY 241 GAGAGVLPVCGVAGVPGVPGAIPIGIGTAGVGTAAAAAAYKAAKAGLVPGG 300  
 DB 241 GAGAGVLPVCGVAGVPGVPGAIPIGIGTAGVGTAAAAAAYKAAKAGLVPGG 300

QY 301 PFGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360  
 DB 301 PFGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360

QY 361 PGVGGVGTPTGYGVAGGFFPGVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420  
 DB 361 PGVGGVGTPTGYGVAGGFFPGVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420

QY 421 AKAAKYGTPTAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 480  
 DB 421 AKAAKYGTPTAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 480

QY 481 VGVAPGVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515  
 DB 481 VGVAPGVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515

RESULT 6  
 AAY69068  
 ID AAY69068 standard; protein; 731 AA.  
 XX

AC AAY69068;  
 XX  
 DT 30-MAY-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human tropoelastin splice form.  
 XX  
 KW Tropoelastin, derivative; proteolysis; protease; antiwrinkle;  
 XX Hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;  
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 441..442  
 FT Cleavage-site 503..504  
 FT Cleavage-site 515..516  
 FT Cleavage-site 564..565  
 XX  
 PN W0200004043-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 19-JUL-1999; 99WO-AU000580.  
 XX  
 PR 17-JUL-1998; 98AU-00004723.  
 XX  
 PA (UNSY ) UNIV SYDNEY.  
 XX  
 PI Weiss AS;  
 XX  
 DR WPI: 2000-182399/16.  
 XX  
 PT N-PSDB; AAK61146.  
 XX  
 PS New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.  
 XX  
 PS Disclosure; Page 107-109; 136pp; English.  
 XX  
 CC The present sequence represents a human tropoelastin splice form. The specification describes tropoelastin derivatives, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

Query Match 100.0%; Score 2680; DB 3; Length 731;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-153;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVPGVPGAGLGGALGGALGGKPLKVPVGGLAGAGLGAFFPAVT 60  
 DB 1 GGVPGAIPGGVPGGVPGVPGAGLGGALGGALGGKPLKVPVGGLAGAGLGAFFPAVT 60

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPPQAGVKPKVPGVGL 120  
 DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPPQAGVKPKVPGVGL 120

QY 121 PGVYPGGVLPGARFFPGVGLPGVPTGAGVKPKAGVGGAGAGVPGVGGVAGVPPQAGVKPKVPGVGL 180  
 DB 121 PGVYPGGVLPGARFFPGVGLPGVPTGAGVKPKAGVGGAGAGVPGVGGVAGVPPQAGVKPKVPGVGL 180





XX	ABG75223;
XX	AC
XX	DT
XX	DE
XX	Human tropoelastin protein.
XX	Human; tropoelastin; elastin; body vessel occlusion; stenosis;
KW	vascular smooth muscle cell; elastin signaling; vasotropic.
KW	XX
OS	Homo sapiens.
OS	WO2003082203-A2.
PN	XX
XX	09-OCT-2003.
PD	XX
XX	27-MAR-2003; 2003WO-USO09391.
PF	XX
XX	27-MAR-2002; 2002US-0368084P.
PR	XX
XX	(UTAH ) UNIV UTAH RES FOUND.
PA	XX
XX	Li DY, Karnik S;
PI	XX
XX	WPI; 2003-833516/77.
DR	XX
XX	use of an agent that promotes elastin signaling in smooth muscle cells
PT	for e.g. decreasing or preventing occlusion of a body vessel by smooth
PT	muscle cells, treating or preventing obstructive vascular disease, or
PT	preventing stenosis.
PT	Claim 24; Page 138-141; Opp: English.
XX	The present invention relates to the use of an agent that promotes
CC	elastin signaling in smooth muscle cells for decreasing or preventing
CC	occlusion of a body vessel by smooth muscle cells, decreasing vascular
CC	obstruction, promoting actin stress fiber formation or actin
CC	polymerisation, increasing F-G actin ratio in a smooth muscle cell,
CC	treating or preventing obstructive vascular disease (e.g. restenosis), or
CC	preventing stenosis. The agent that promotes elastin signaling in smooth
CC	muscle cells is useful for decreasing or preventing occlusion of a body
CC	vessel by smooth muscle cells, decreasing vascular obstruction, promoting
CC	actin stress fiber formation or actin polymerization, increasing F:G
CC	actin ratio in a smooth muscle cell, treating or preventing obstructive
CC	vascular disease (e.g. restenosis following angioplasty), or preventing
CC	stenosis. It is also useful in manufacturing a medicament for the
CC	treatment or prevention of occlusion of a vessel. The present sequence is
CC	the human tropoelastin protein as shown in the exemplification of the
CC	invention
XX	Sequence 757 AA;
SQ	Query Match 100.0%; Score 2680; DB 7; Length 757;
	Best Local Similarity 100.0%; Pred. No. 7.6e-153;
	Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GGVPICALPGGVGGVFYPGAGLGAALGGALPGCGKLPVPGGLAAGLGAGLGAFFAVT 60
Dd	27 GGVGPALPEGVGPGGVFPFGAGLGGALPGGKPLKPVPGGLAAGLGAGLGAFFAVT 86
QY	61 PFGLVPCGVADAAAAAYAAKAKAGLAGLGGVFPVGVLGVSAGAVVPOGAGVKPKVPGVL 120
Dd	87 PFGLVPCGVADAAAAAYAAKAKAGLAGLGGVFPVGVLGVSAGAVVPOGAGVKPKVPGVL 146
QY	121 PGVYFPGVLPGARFPGVGLPVGVTGAGVKFKAPGVGGAFAGIPGVPGGPPQGVPLGY 180
Dd	147 PGVYFPGVLPGARFPGVGLPVGVTGAGVKEFAFVGGAFAPIPVGFPFGPPQGVPLGY 206
QY	181 PIKAPKLPGGYGLPYTTGKLPYGVPFGVAGAAGKAGYPTGTGVCAPAAAATAAKAAKF 240
Dd	207 PIKAPKLPGGYGLPYTTGKLPYGVPFGVAGAAGKAGYPTGTGVCAPAAAATAAKAAKF 266
QY	241 GAGAAGVLPVGVGAGVPGVPGAIPGIIGIAGVGTTPAAAAATAAKAAKYGAAAGLVPGG 300

Db	267	GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTAAAAAAXAAKATGAAGLVPGG	326
Qy	301	PGFGPGVVGVPVGGAGVPGVPGAGIPVPGAGIPGAAPVGVSPVPEAAKAAKAAKATGAG	360
Db	327	PGFGPGVVGVPVGGAGVPGVPGAGIPVPGAGIPGAAPVGVSPVPEAAKAAKAAKATGAG	386
Qy	361	PGVGVGGIPVPGVGGAGVPGVPGVGGIPVGVAGVPSVGGVPGVGGVPGVPGVSPVPEAAKAA	420
Db	387	PGVGVGGIPTVGVGGAGVPGVPGVGGIPVGVAGVPSVGGVPGVGGVPGVPGVSPVPEAAKAA	446
Qy	421	AKAAKYGVTAAAAAAXAAKAAKAAQFGLVPGVGVAPGVGVAGVPGVPGVPGVPGVPGV	480
Db	447	AKAAKYGVTAAAAAAXAAKAAKAAQFGLVPGVGVAPGVGVAGVPGVPGVPGVPGVPGV	506
Qy	481	VGVAPGVGVAPGVGGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA	515
Db	507	VGVAPGVGVAPGVGGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA	541
RESULT	11		
ADP65160			
ID	ADP65160	standard; protein; 757 AA.	
XX	AC	ADP65160;	
XX	XX	12-AUG-2004 (first entry)	
DT	XX	Human elastin.	
DE	XX	autoimmune disease; arthritis; gene expression analysis;	
XX	KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;	
KW	KW	antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;	
KW	KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;	
KW	KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;	
XX	XX	immune; human.	
OS	XX	Homo sapiens.	
XX	XX	WO2003072827-A1.	
FN	XX	04-SEP-2003.	
XX	XX	31-OCT-2002; 2002WO-US035433.	
PF	XX	31-OCT-2001; 2001US-0336220P.	
PR	XX	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.	
PA	XX	Hirsch R, Thorton SL;	
PI	XX	WPI; 2003-712740/67.	
DR	XX	GENBANK; NP_000492.	
XX	XX	Diagnosing and analyzing autoimmune disease using gene expression	
PT	PT	profiles and microarray technology, useful for diagnosing and treating	
PT	PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and	
PT	PT	gout.	
XX	XX	Disclosure; Page; 56pp; English.	
XX	XX	The invention relates to a novel method for diagnosing and analysing a	
CC	CC	autoimmune disease or arthritides. The method comprises obtaining a	
CC	CC	patient sample containing mRNA, analysing gene expression using the mRNA	
CC	CC	that results in a gene expression signature of the mRNA, and using that	
CC	CC	gene expression signature to diagnose or analyse the autoimmune disease	
CC	CC	or arthritides in the patient, where gene expression of at least 60% of	
CC	CC	the genes correlates with that of the gene signature. The invention	
CC	CC	further comprises: a treatment of rheumatoid arthritis; identification of	
CC	CC	genes for targeting in the treatment of rheumatoid arthritis in a mamma	
CC	CC	other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an	
CC	CC	array or gene chip, specific for rheumatoid arthritis; diagnosis or	
CC	CC	analyses of autoimmune disease or rheumatoid arthritis; screening the	

CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, anti-rheumatic, anti-arthritis, osteopathic,  
 CC antigout, anti-inflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritis, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This sequence represents a  
 CC protein sequence relating to the genes used in the analysis and treatment  
 CC of autoimmune diseases or arthritis. Note: This sequence is not shown  
 CC in the specification. It has been supplied in an electronic format from  
 CC WIPO.

XX Sequence 757 AA;

Query Match 100.0%; Score 2680; DB 7; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-153;  
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVYFPGAGLGGGALGGGKPLKPVPGGLAGAGLGAFFAVT 60  
 Db 27 GGVPGAIPGGVPGGVYFPGAGLGGGALGGGKPLKPVPGGLAGAGLGAFFAVT 86

QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVSGAGAVVPPQAGVPGKVPVGL 120  
 Db 87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGLGVSGAGAVVPPQAGVPGKVPVGL 146

QY 121 PGVTPGGVLPGARFPFGVLPVGTAGVKPKAGVGGAGAGIPGVPGPQPGVPLGY 180  
 Db 147 PGVTPGGVLPGARFPFGVLPVGTAGVKPKAGVGGAGAGIPGVPGPQPGVPLGY 206

QY 181 PIKAPKLPGGVGLPYTTGKLPYGVGGVAGAGKAGYPTGTGVPQAAAAAKAAKF 240  
 Db 207 PIKAPKLPGGVGLPYTTGKLPYGVGGVAGAGKAGYPTGTGVPQAAAAAKAAKF 266

QY 241 GAGAAGVLPGGVAGVPGVPGAGIPVPGAGIPGAAPGVSPVSPVSPVSPVSPVSPV 300  
 Db 267 GAGAAGVLPGGVAGVPGVPGAGIPVPGAGIPGAAPGVSPVSPVSPVSPVSPV 326

QY 301 PGFGVGGVPGVAGVPGVPGAGIPVPGAGIPGAAPGVSPVSPVSPVSPVSPVSPV 360  
 Db 327 PGFGVGGVPGVAGVPGVPGAGIPVPGAGIPGAAPGVSPVSPVSPVSPVSPV 386

QY 361 PGVGVGGIPTYGVAGGFFGFGVGGIPGVAGVSPVSPVSPVSPVSPVSPVSPV 420  
 Db 387 PGVGVGGIPTYGVAGGFFGFGVGGIPGVAGVSPVSPVSPVSPVSPVSPVSPV 446

QY 421 AKAAKYGVTTPAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 480  
 Db 447 AKAAKYGVTTPAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 506

QY 481 VGVAPGVGVPAGIPGGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 515  
 Db 507 VGVAPGVGVPAGIPGGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 541

RESULT 12

ADL96420  
 ID ADL96420 standard; protein; 731 AA.

XX AC ADL96420;

XX DT 20-MAY-2004 (first entry)

XX DE Human elastin protein fragment.

XX KW fibrous protein; prosthesis; elastin; lamprin; spider silk protein;  
 KW blood vessel; wound; burn healing; collagen.

XX OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Region 19..160  
 FT /note="region specifically claimed in claim 6"  
 FT Region 188..367  
 FT /note="region specifically claimed in claim 6"  
 FT Region 374..499  
 FT /note="region specifically claimed in claim 6"  
 FT Region 607..717  
 FT /note="region specifically claimed in claim 6"  
 XX US2003166846-A1.  
 XX PD 04-SEP-2003.  
 XX PF 28-SEP-2001; 2001US-00964662.  
 PR 07-AUG-1996; 96US-0023522P.  
 PR 07-AUG-1997; 97US-00911364.  
 PR 29-JUN-1999; 99US-00340736.  
 XX (ROTH/) ROTHSTEIN A.  
 PA (KEEL/) KEELEY F.  
 PA (ROTH/) ROTHSTEIN S.  
 PI Rothstein A, Keeley F, Rothstein S;  
 DR WPI; 2003-898105/82.  
 PT Polypeptide for constructing human elastin-like prostheses such as tubes  
 PT for blood vessel replacement and sheets for other uses such as wound or  
 PT burn healing, comprises three beta sheets and three beta turns.  
 PS Claim 5; Fig 1B; 17pp; English.

This invention describes a polypeptide that comprises three beta sheet/beta turn structures and that is not a naturally occurring fibrous protein. The invention also describes a prosthesis comprising an animal, metal or synthetic material, where the surface is coated with the polypeptide, a cosmetic material comprising the polypeptide, an elastic material comprising the polypeptide, a high tensile strength material comprising the polypeptide, a material comprising two or more polypeptides selected from (a) a polypeptide consisting essentially of a portion of the polypeptide comprising at least three beta sheet/beta turn structures, (b) a polypeptide consisting essentially of a portion of the amino acid sequence of an animal elastin comprising at least three beta sheets/beta turns, (c) a polypeptide consisting essentially of a portion of lamprin comprising at least three beta sheets/beta turns, and (d) a polypeptide consisting essentially of a spider silk protein comprising at least three beta sheets/beta turns, a polypeptide having the primary structure of a portion of a naturally occurring fibrous protein and a secondary structure comprising at least three beta sheets/beta turns, where each of the beta sheet/beta turn structures comprises from 3 to about 7 amino acids and the polypeptide is not a naturally occurring fibrous protein. The minimal functional unit (MFU) of the invention is useful to construct human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing. Alternatively the MFU can be co-aggregated with other proteins, for example collagen, to provide prosthesis material that resembles the natural structural materials of the body. The MFU based material is subject to infiltration of cells growing in the patient, including endothelial cells, and the prosthesis can become a permanent living tissue replacement. The material is more biocompatible than other elastin -containing materials proposed for prostheses.

XX Sequence 731 AA;

Query Match 99.7%; Score 2672; DB 7; Length 731;  
 Best Local Similarity 99.8%; Pred. No. 2.2e-152;  
 Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVYFPGAGLGGGALGGGKPLKPVPGGLAGAGLGAFFAVT 60  
 Db 1 GGVPGAIPGGVPGGVYFPGAGLGGGALGGGKPLKPVPGGLAGAGLGAFFAVT 60

XX	Claim 1; Fig 1B; 21pp; English.	
PS	The invention describes a polypeptide (1) comprising a minimal	
XX	functioning unit (MFU) which is present in the sequence of human elastin	
CC	and comprised of at least three beta-sheet/beta-turn structures, and at	
CC	least one amino acid residue that participates in cross-linking, and not	
CC	a naturally occurring fibrous protein. The MFU material can be used to	
CC	construct human elastin-like prostheses such as tubes for blood vessel	
CC	replacement, heart replacement valves and sheets for other uses such as	
CC	burns or wounds to promote healing. MFUs can be co-aggregated with other	
CC	proteins, for e.g. collagen, to provide prosthesis material that	
CC	resembles the natural structural materials of the body. MFUs modeled on	
CC	lamprin and other fibrous proteins e.g. spider silk, can be used to make	
CC	in cords and ropes for use in parachutes and in cosmetics. Coating	
CC	synthetic prosthesis with MFUs modeled on human elastin significantly	
CC	inhibits platelet binding and activation. The human-like MFU material is	
CC	more biocompatible than other elastin-containing materials. In contrast	
CC	to solubilised fragments of elastin used before, an MFU is a single	
CC	peptide of defined composition. The MFU is considerably smaller than the	
CC	parent protein, simpler in structure, easier to produce or express in	
CC	quantity, to handle in solution and to manipulate for experimental and	
CC	practical purposes. Like other elastin preparations, the MFU is non-	
CC	thrombogenic and provides a friendly environment for cell infiltration.	
CC	Being composed entirely of a human elastin sequence, MFU is non-	
CC	immunogenic, thus providing a truly biocompatible material. MFUs modeled	
CC	on lamprin and other fibrous proteins can be used to make a variety of	
CC	materials having high tensile strength, elasticity and plasticity of	
CC	their parent proteins. This is the amino acid sequence of mature human	
CC	elastin on which the MFU peptides of the invention are based	
XX	Sequence 731 AA;	
SQ	Query Match 99.6%; Score 2670; DB 6; Length 731;	
	Best Local Similarity 99.6%; Pred. No. 2.9e-152;	
	Matches 513; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 GGVPGAIPGGVPGVFPYAGI	GALGGALGPGGKPLKPVPGGLAGAGLGAAPAVT 60
Db	1 GGVPGAIPGGVPGVFPYAGI	GALGGALGPGGKPLKPVPGGLAGAGLGAAPAVT 60
QY	61 FPGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPQAGVKKPKVPGVGL 120	
Db	61 FPGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPQAGVKKPKVPGVGL 120	
QY	121 PGVYPGVLPGARFPVGGVLPVGVPTGAGVKKPKAPGVGGAFAGIPGVGPGPGVPLGY 180	
Db	121 PGVYPGVLPGARFPVGGVLPVGVPTGAGVKKPKAPGVGGAFAGIPGVGPGPGVPLGY 180	
QY	181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240	
Db	181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240	
QY	241 GAGAAGVLPVGGVAGVPGVGAIPGIGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 300	
Db	241 GAGAAGVLPVGGVAGVPGVGAIPGIGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 300	
QY	301 PGFPGVVGVPAGVPGVPGAGIPVVPAGIPGAAPGVVSPPEAAKAAKAYGAR 360	
Db	301 PGFPGVVGVPAGVPGVPGAGIPVVPAGIPGAAPGVVSPPEAAKAAKAYGAR 360	
QY	361 PGVGGIPTYGVGAGGPGFPGVGGIPGVAGVPSVGGVPGVGGVPGVGI SPFAQAAA 420	
Db	361 PGVGGIPTYGVGAGGPGFPGVGGIPGVAGVPSVGGVPGVGGVPGVGI SPFAQAAA 420	
QY	421 AKAAKYGVGTTPAAAAAATAAKAAQFGLVPGVAGVPGVAGVPGVGLAPGVGAPG 480	
Db	421 AKAAKYGVGTTPAAAAAATAAKAAQFGLVPGVAGVPGVAGVPGVGLAPGVGAPG 480	
QY	481 VGVAFGVGVAPGIGPGGVAAAAAATAAKAAKAAQRLR 515	
Db	481 VGVAFGVGVAPGIGPGGVAAAAAATAAKAAKAAQRLR 515	

XX	61 FPGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPQAGVKKPKVPGVGL 120
XX	61 FPGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPQAGVKKPKVPGVGL 120
QY	121 PGVYPGVLPGARFPVGGVLPVGVPTGAGVKKPKAPGVGGAFAGIPGVGPGPGVPLGY 180
Db	121 PGVYPGVLPGARFPVGGVLPVGVPTGAGVKKPKAPGVGGAFAGIPGVGPGPGVPLGY 180
QY	181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240
Db	181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240
QY	241 GAGAAGVLPVGGVAGVPGVGAIPGIGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 300
Db	241 GAGAAGVLPVGGVAGVPGVGAIPGIGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 300
QY	301 PGFPGVVGVPAGVPGVPGAGIPVVPAGIPGAAPGVVSPPEAAKAAKAYGAR 360
Db	301 PGFPGVVGVPAGVPGVPGAGIPVVPAGIPGAAPGVVSPPEAAKAAKAYGAR 360
QY	361 PGVGGIPTYGVGAGGPGFPGVGGIPGVAGVPSVGGVPGVGGVPGVGI SPFAQAAA 420
Db	361 PGVGGIPTYGVGAGGPGFPGVGGIPGVAGVPSVGGVPGVGGVPGVGI SPFAQAAA 420
QY	421 AKAAKYGVGTTPAAAAAATAAKAAQFGLVPGVAGVPGVAGVPGVGLAPGVGAPG 480
Db	421 AKAAKYGVGTTPAAAAAATAAKAAQFGLVPGVAGVPGVAGVPGVGLAPGVGAPG 480
QY	481 VGVAFGVGVAPGIGPGGVAAAAAATAAKAAKAAQRLR 515
Db	481 VGVAFGVGVAPGIGPGGVAAAAAATAAKAAKAAQRLR 515

RESULT 13

ABU08725

ID ABU08725 standard; protein; 731 AA.

XX AC ABU08725;

XX XX 25-JUN-2003 (first entry)

DT XX Human elastin mature protein.

DE XX Human; elastin; minimal functioning unit; MFU;

XX KW beta-sheet/beta-turn structure; fibrous protein; prosthesis;

KW KW blood vessel replacement; heart replacement valve; burn; wound; lamprin;

KW KW spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;

KW KW platelet activation inhibitor; non-thrombogenic; cell infiltration;

KW KW non-immunogenic; biocompatible; high tensile strength; elasticity;

XX KW plasticity.

OS Homo sapiens.

XX OS US6489446-B1.

PN XX 03-DEC-2002.

ED XX 29-JUN-1999; 99US-00340736.

XX PF 07-AUG-1996; 96US-0023522P.

XX PR 07-AUG-1997; 97US-00911364.

XX XX (HSCR-) HSC RES & DEV LP.

PA (PROT-) PROTEIN SPECIALTIES LTD.

XX XX Rothstein A, Keeley F, Rothstein S;

XX XX WPI; 2003-391056/37.

DR XX Novel polypeptide useful in prosthesis, has a secondary structure

PT PT characterized by three beta-sheet/beta-turn structures, and is not a

PT PT naturally occurring fibrous protein.

RESULT 14  
 ADE40132  
 ID ADE40132 standard; protein; 711 AA.  
 XX  
 AC ADE40132;  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOV16a protein - SEQ ID 38.  
 XX  
 KW NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
 KW antiatherogenic; immunosuppressive; anti-HIV; neuroprotective; anorectic;  
 KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;  
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
 KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
 KW tissue typing; human; NOV.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003064589-A2.  
 XX  
 PD 07-AUG-2003.  
 XX  
 PF 02-AUG-2002; 2002WO-US024483.  
 XX  
 PR 02-AUG-2001; 2001US-0309501P.  
 PR 03-AUG-2001; 2001US-0310291P.  
 PR 07-AUG-2001; 2001US-0310544P.  
 PR 08-AUG-2001; 2001US-0310951P.  
 PR 09-AUG-2001; 2001US-0311292P.  
 PR 13-AUG-2001; 2001US-0311979P.  
 PR 16-AUG-2001; 2001US-0312892P.  
 PR 17-AUG-2001; 2001US-0313201P.  
 PR 20-AUG-2001; 2001US-0313415P.  
 PR 20-AUG-2001; 2001US-0313643P.  
 PR 21-AUG-2001; 2001US-0313702P.  
 PR 23-AUG-2001; 2001US-0314031P.  
 PR 28-AUG-2001; 2001US-0314466P.  
 PR 29-AUG-2001; 2001US-0315403P.  
 PR 17-SEP-2001; 2001US-0315853P.  
 PR 21-SEP-2001; 2001US-0322716P.  
 PR 14-DEC-2001; 2001US-0323994P.  
 PR 05-FEB-2002; 2001US-0340233P.  
 PR 19-MAR-2002; 2002US-0354591P.  
 PR 19-APR-2002; 2002US-0365478P.  
 PR 19-APR-2002; 2002US-0373814P.  
 PR 19-APR-2002; 2002US-0373825P.  
 PR 23-APR-2002; 2002US-0373989P.  
 PR 07-JUN-2002; 2002US-0374632P.  
 PR 01-AUG-2002; 2002US-0386971P.  
 XX  
 (CURA-) CURAGEN CORP.  
 XX  
 FI Kekuda R, Miller CE, Patturajan M, Pena CE, Rieger DK;  
 PI Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;  
 PI Voss EZ, Boldog FI, Gorman L, Leite MW, Vernet CAM, Anderson DW;  
 PI Guo X, Zhong M, Gerlach VL, Hjalte T, Rastelli L, Spytek KA;  
 PI Edinger SR, Ellerman K, Malyankar UM, MacDougall JR, Stone DU;  
 PI Alsbrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;  
 PI Smithson G;  
 XX  
 WPI; 2003-663472/62.  
 DR N-PSDB; ADE40131.  
 DR  
 XX  
 PT New NOVX polypeptides and nucleic acids, useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX



KW platelet derived growth factor receptor alpha; laminin M chain;  
 KW subtilisin like protein PACB4; nidogen.  
 OS Homo sapiens.  
 XX EF1191107-A2.  
 XX PD 27-MAR-2002.  
 XX 21-AUG-2001; 2001EP-00250300.  
 XX 25-SEP-2000; 2000DE-01048633.  
 XX (SCHD ) SCHERING AG.  
 XX Hess-Stumpff H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;  
 PI Regidor P, Scotti S;  
 XX WPI; 2002-317413/36.  
 DR In vitro diagnosis and monitoring of endometriosis, comprises detecting  
 XX reduced expression of specific gene products, e.g. from the fibronectin  
 PT gene.  
 XX Claim 1; Page 15-16; 21pp; German.

XX The present invention relates to a method for the in vitro diagnosis of  
 CC endometriosis by determining the amount of gene product from at least one  
 CC specific gene in a patient sample and comparing this with the amount of  
 CC gene product in a control sample. A reduced level is indicative of  
 CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,  
 CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,  
 CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,  
 CC transmembrane receptor PK7, collagen type XVIII alpha 1, platelet  
 CC derived growth factor receptor alpha, laminin M chain, subtilisin like  
 CC protein PACB4 or nidogen. The method is useful for initial diagnosis of  
 CC endometriosis, and also for monitoring progress and treatment of the  
 CC disease. The present sequence is human elastin  
 XX

XX SQ Sequence 730 AA;

Query Match 99.5%; Score 2667; DB 5; Length 730;  
 Best Local Similarity 98.8%; Pred. No. 4.4e-152;  
 Matches 515; Conservative 0; Mismatches 0; Indels 6; Gaps 1;  
 1 GGVPGAIPGGVPGGVFYPGAGLGGALGGALGGKPLKPVPGGLAGAGLGAFAFPAVT 60  
 27 GGVPGAIPGGVPGGVFYPGAGLGGALGGALGGKPLKPVPGGLAGAGLGAFAFPAVT 86  
 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLVGSAGAVVPPQAGVPGKVPVGL 120  
 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLVGSAGAVVPPQAGVPGKVPVGL 146  
 121 PGVYPGVLPGARFPGVGLVPGVTPAGVKAFAAGVAGAFAGIPGVGPFPGQVPLGY 180  
 147 PGVYPGVLPGARFPGVGLVPGVTPAGVKAFAAGVAGAFAGIPGVGPFPGQVPLGY 206  
 181 PIKAPKLPGGVGLPYTTCKLPYGGVPGGVAGAGKAGVPTGTGVPQAAAAAAYKAAKAF 240  
 207 PIKAPKLPGGVGLPYTTCKLPYGGVPGGVAGAGKAGVPTGTGVPQAAAAAAYKAAKAF 266  
 241 GAGAGVLPVGGAGVPGVPGAIPGIGGAGVGTTPAAAAAAYKAAKAGVAGAGVPGG 300  
 267 GAGAGVLPVGGAGVPGVPGAIPGIGGAGVGTTPAAAAAAYKAAKAGVAGAGVPGG 326  
 301 PGFPGVGVPGAGVPGVPGAIPVPGAGIPGAAVPGVSPAAAAAAYKAAKAGVAGAR 360  
 327 PGFPGVGVPGAGVPGVPGAIPVPGAGIPGAAVPGVSPAAAAAAYKAAKAGVAGAR 386  
 361 PGVGVGSIPTYGVGAGFPFGVGVGIPGVAGVPSVGGVPGVGGVPGVGVISPEAQA 420  
 387 PGVGVGSIPTYGVGAGFPFGVGVGIPGVAGVPSVGGVPGVGGVPGVGVISPEAQA 446

QY 421 AKAAKYGVTGTPAAAAAAYKAAKAGAF-----GLVPGVPGVAPGVGVPAGVGLAPG 474  
 DB 447 AKAAKYGVTGTPAAAAAAYKAAKAGAF-----GLVPGVPGVAPGVGVPAGVGLAPG 506  
 QY 475 VGVAPGVGVPAGVPGVAPGIPGPGVAAAAAAYKAAKAGVAGAR 515  
 DB 507 VGVAPGVGVPAGVPGVAPGIPGPGVAAAAAAYKAAKAGVAGAR 547

RESULT 16

ADQ19747 ADQ19747 standard; protein; 730 AA.

XX AC ADQ19747;

XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 XX Example 2; SEQ ID NO 2566; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual,  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytostatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 CC acid sequences may be useful in diagnostic and screening applications.  
 CC The current sequence is that of a human soft tissue sarcoma-upregulated  
 CC protein of the invention. The current sequence is not shown within the  
 CC specification per se but was submitted in CD format by the inventor.

XX SQ Sequence 730 AA;

Query Match 99.5%; Score 2667; DB 8; Length 730;  
 Best Local Similarity 98.8%; Pred. No. 4.4e-152;  
 Matches 515; Conservative 0; Mismatches 0; Indels 6; Gaps 1;  
 1 GGVPGAIPGGVPGGVFYPGAGLGGALGGALGGKPLKPVPGGLAGAGLGAFAFPAVT 60  
 27 GGVPGAIPGGVPGGVFYPGAGLGGALGGALGGKPLKPVPGGLAGAGLGAFAFPAVT 86  
 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLVGSAGAVVPPQAGVPGKVPVGL 120  
 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLVGSAGAVVPPQAGVPGKVPVGL 146  
 121 PGVYPGVLPGARFPGVGLVPGVTPAGVKAFAAGVAGAFAGIPGVGPFPGQVPLGY 180



Db	147	PGVYPGVLPGARFFPGVGVLPGVPTGAGVKPAPGVGSAFAGIPGVPGPGQPGVPLGY	206
QY	181	PIKAPKLPGGYGLPYTTGKLPYGVGPGGVAGAGKAGYPTGTGVPQAAAAKAAAKF	240
Db	207	PIKAPKLPGGYGLPYTTGKLPYGVGPGGVAGAGKAGYPTGTGVPQAAAAKAAAKF	266
QY	241	GAGAAAGVLPVGGAGVPGVPGAIPIGIGGIAGVGTFAAAAAAAXKAAAGLVPGG	300
Db	267	GAGAAAGVLPVGGAGVPGVPGAIPIGIGGIAGVGTFAAAAAAAXKAAAGLVPGG	326
QY	301	PGFGPGVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPAAAAKAAAKYGAR	360
Db	327	PGFGPGVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPAAAAKAAAKYGAR	386
QY	361	PGVGVGGIPTTYGVGAGGPFPGVGVGGIPGVAGVPSGVGPGVGVGVTSPAAAAA	420
Db	387	PGVGVGGIPTTYGVGAGGPFPGVGVGGIPGVAGVPSGVGPGVGVGVTSPAAAAA	446
QY	421	AKAAKYGVGTFAAAAAKAAAKAAQF-----GLVPGVGPVPGVGPVGPVGLAPG	474
Db	447	AKAAKYGVGTFAAAAAKAAAKAAQFALLNLAGLVPGVGPVGPVGPVGPVGLAPG	506
QY	475	VGVAPGVGVPFPGVGPVPGIGIPGGVAAAAKSAAKVAAQAQLR	515
Db	507	VGVAPGVGVPFPGVGPVPGIGIPGGVAAAAKSAAKVAAQAQLR	547

RESULT 17  
 AAB08630  
 ID AAB08630 standard; peptide; 712 AA

## RESULT 17

AA080630	
ID	AA080630 standard; peptide; 712 AA.
XX	
AC	AA080630;
XX	
DT	20-DEC-2000 (first entry)
XX	
DE	Amino acid sequence of a human elastin polypeptide.
XX	
KW	Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW	smooth muscle cell differentiation; smooth muscle cell migration;
KW	smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW	vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW	SVAS; hypertension; transplant arteriopathy.
XX	
OS	Homo sapiens.
XX	
W0	W0200050068-A2.
XX	
31	31-AUG-2000.
XX	
28	28-FEB-2000; 2000WO-US002526.
XX	
26	26-FEB-1999; 99US-00258217.
XX	
(UTAH	) UNIV UTAH RES FOUND.
XX	
Keating	MT, Li DY;
XX	
WPI;	2000-533134/48.
XX	
Elastin	based compositions useful for treating atherosclerosis,
XX	restenosis, vascular bypass graft stenosis, transplant arteriopathy,
XX	aneurysm, dissection SVAS and/or hypertension.
XX	
Example	3; Page 46; 79pp; English.
XX	
The	present sequence represents a human elastin. Peptides derived from
XX	elastin are used in compositions of the invention. The specification
XX	describes elastin based compositions that are potent regulators of smooth
XX	muscle cell proliferation, differentiation and migration in vivo. The
XX	elastin-based compositions comprise at least one elastic fibre, elastins
XX	tropoelastins (or fragments of them) which have biological activities
XX	comprising: inhibiting the proliferation of smooth muscle cells in vivo;

Mon Nov 22 12:42:42 2004

31-AUG-2000.  
28-FEB-2000; 2000WO-US002526.  
26-FEB-1999; 99US-00258217.  
(UTAH ) UNIV UTAH RES FOUND.  
Keating MT, Li DY;  
WPI; 2000-533134/48.  
Elastin based compositions useful for treating atherosclerosis,  
restenosis, vascular bypass graft stenosis, transplant arteriopathy,  
aneurysm, dissection SVAs and/or hypertension.  
Example 3; Page 48; 79pp; English.  
The present sequence represents a fusion protein, comprising human  
elastin and c-myc, preceded by a His tag. The protein is used in  
compositions of the invention. The specification describes elastin based  
compositions that are potent regulators of smooth muscle cell  
proliferation, differentiation and migration in vivo. The elastin-based  
compositions comprise at least one elastic fibre, elastins, tropoelastins  
(or fragments of them) which have biological activities comprising:  
inhibiting the proliferation of smooth muscle cells in vivo; stimulating  
the differentiation of smooth muscle cell in vivo; and regulating the  
migration of smooth muscle cells in vivo. The compositions may be used  
for the prophylaxis or treatment of a disorder characterized by  
diminished capacity to regulate smooth muscle cell function such as  
atherosclerosis, restenosis, vascular bypass graft stenosis, transplant  
arteriopathy, aneurysm and/or dissection. Disorders which may be treated  
also include SVAs (undefined), hypertension, and transplant arteriopathy  
SQ Sequence 730 AA;  
Query Match 99.4%; Score 2663; DB 3; Length 730;  
Best Local Similarity 98.7%; Pred. No. 7.7e-152;  
Matches 514; Conservative 0; Mismatches 1; Indels 6; Gaps 1;  
1 GGVPGAIPGGVPGGVPGAGLGGALGGALGGKPLKVPVGGLAGAGLGGAGLGAFFAVT 60  
36 GGVPGAIPGGVPGGVPGAGLGGALGGALGGKPLKVPVGGLAGAGLGGAGLGAFFAVT 95  
61 FGALVPGGVADAAAAAAYAAKAGAGLGGVPGVGGVGSAGAVPQPAGVKKVPVGVGL 120  
96 FGALVPGGVADAAAAAAYAAKAGAGLGGVPGVGGVGSAGAVPQPAGVKKVPVGVGL 155  
121 PGVVPGGVLPGARFPGGVLPVPGVTPGAKPAGVGGAGFAGIPGVPGPGPQGVPLGY 180  
156 PGVVPGGVLPGARFPGGVLPVPGVTPGAKPAGVGGAGFAGIPGVPGPGPQGVPLGY 215  
181 PIKAPKLPGGVGLPYTTTKLPGVGGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 240  
216 PIKAPKLPGGVGLPYTTTKLPGVGGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 275  
241 GAGAAGVLPVGGAGVPGVPGAGIPGIGGAGVGTPTAAAAAATAAKAYGAAGLVPGG 300  
276 GAGAAGVLPVGGAGVPGVPGAGIPGIGGAGVGTPTAAAAAATAAKAYGAAGLVPGG 335  
301 PGFGGVVPGVPGAGVPGVPGAGIPVPGAGIPGAAPVGVVSPAAAAAATAAKAYGAR 360  
336 PGFGGVVPGVPGAGVPGVPGAGIPVPGAGIPGAAPVGVVSPAAAAAATAAKAYGAR 395  
361 PCVGVGGIPVPGVGGAGFPFGVGGVPGVAGVSPVGGVPGVGGVPGVGTSPAAAAA 420  
396 PGVGVGGIPVPGVGGAGFPFGVGGVPGVAGVSPVGGVPGVGGVPGVGTSPAAAAA 455  
421 AKAAYGVGTPTAAAAAATAAKAQAQF-----GLVPGVGVAPGVGVAPGVGLAPG 474  
456 AKAAYGVGTPTAAAAAATAAKAQAQFALLNLGLVPGVGVAPGVGVAPGVGLAPG 515  
475 VGVPAGVGVAPGVGVAPGVPGIPGGVAAAAAASAKVAQAQLR 515

516 VGVPAGVGVAPGVGVAPGVPGIPGGVAAAAAASAKVAQAQLR 556

Db

RESULT 19

ADE40134

ID ADE40134 standard; protein; 692 AA.

XX AC ADE40134;

XX AC ADE40134;

DT 29-JAN-2004 (first entry)

DE Human NOV16b protein - SEQ ID 40.

XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
XX anti-diabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;  
XX antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;  
XX atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;  
XX multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;  
XX asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;  
XX tissue typing; human; NOV.

XX Homo sapiens.

OS WO2003064589-A2.

PN 07-AUG-2003.

XX 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

XX 03-AUG-2001; 2001US-0310291P.

XX 07-AUG-2001; 2001US-0310544P.

XX 08-AUG-2001; 2001US-0310951P.

XX 09-AUG-2001; 2001US-0311292P.

XX 13-AUG-2001; 2001US-0311979P.

XX 16-AUG-2001; 2001US-0312892P.

XX 17-AUG-2001; 2001US-0313201P.

XX 17-AUG-2001; 2001US-0313415P.

XX 20-AUG-2001; 2001US-0313643P.

XX 20-AUG-2001; 2001US-0313702P.

XX 21-AUG-2001; 2001US-0314031P.

XX 23-AUG-2001; 2001US-0314466P.

XX 28-AUG-2001; 2001US-0315403P.

XX 29-AUG-2001; 2001US-0315853P.

XX 17-SEP-2001; 2001US-0322716P.

XX 21-SEP-2001; 2001US-0323944P.

XX 14-DEC-2001; 2002US-0354591P.

XX 05-FEB-2002; 2002US-0365478P.

XX 19-MAR-2002; 2002US-0373814P.

XX 19-APR-2002; 2002US-0373825P.

XX 19-APR-2002; 2002US-0373989P.

XX 23-APR-2002; 2002US-0374632P.

XX 07-JUN-2002; 2002US-0386971P.

XX 01-AUG-2002; 2002US-00210172.

(CURA-) CURAGEN CORP.

Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;

Shinkels RA, Zerhusen BD, Li L, Ji W, Padigar M, Casman SJ;

Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;

Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;

Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;

Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;

Smithson G;

WPI; 2003-663472/62.

N-PSDB; ADE40133.

New NOVX polypeptides and nucleic acids, useful for preventing or  
treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
atherosclerosis or diabetes, and in chromosome mapping, tissue typing or

PT	pharmacogenomics.
XX	Claim 1; SEQ ID NO 40; 560pp; English.
XX	The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC	invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
CC	cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC	neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
CC	gynaecological activities and may be useful in diagnosing, treating or
CC	preventing NOVX-associated disorders including cardiomyopathy,
CC	atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
CC	sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC	disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC	be utilised as vaccines whilst the nucleic acids may be used as
CC	hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC	preventive medicine and pharmacogenomics. The current sequence is that of
CC	the human NOV protein of the invention.
XX	
SQ	Sequence 692 AA;
	Query Match            90.7%; Score 2431; DB 7; Length 692;
	Best Local Similarity   91.6%; Pred. No. 5.9e-138;
	Matches     477; Conservative     0; Mismatches     0; Indels     44; Gaps     2;
QY	1 GGVPGAIPGGVPGGVFPAGLIGALGGGALPGGKPLKPVPGLAGAGLAGAGLCAFAFNAV 60
Dd	27 GGVPGAIPGGVPGGVFPAGLIGALGGGALPGGKPLKPVPGLAGAGLCAFAFNAV 86
QY	61 PFGALVPGGVADAAAYAAKAGAGLGVGPGVGGGLVSAGAVVPPQGAGVKPQVPGVL 120
Dd	87 PFGALVPGGVADAAAYAAKAGAGLGVGPGVGGGLVSAGAVVPPQGAGVKPQV 141
QY	121 PGVYPGGVLPGAEPFGVGVLPQVTPGAGVKPKAPQGVGAFAGIPGVGPFGPGPVPLGY 180
Dd	142 -----PVGGNFAGIPGVGFPGPGPVPLGY 168
QY	181 PIKAPKLPGGYGLPYTTGKLPYGYPGGVAGAAGKAGYPTGTGVGPAAAAAATAAKAF 240
Dd	169 PIKAPKLPGGYGLPYTTGKLPYGYPGGVAGAAGKAGYPTGTGVGPAAAAAATAAKAF 228
QY	241 GAGAGLVLPVGGGAGVPGVPCAIPGIIGIAGVTGTPAAAAAATAAKAGAAAGLVPGG 300
Dd	229 GAGAGLVLPVGGGAGVPGVPCAIPGIIGIAGVTGTPAAAAAATAAKAGAAAGLVPGG 288
QY	301 PGFGPGVVVPGAGVPGVPGAGIPVWPCAGIPGAHVPGVTSPEAAAATAAKAYGAR 360
Dd	289 PGFGPGVVVPGAGVPGVPGAGIPVWPCAGIPGAHVPGVTSPEAAAATAAKAYGAR 348
QY	361 PGVGVGGIPTYGVGAGGPFPGFGVGGGIPGVAGVPSVGGVPGVGGVPGVGISPEACAAA 420
Dd	349 PGVGVGGIPTYGVGAGGPFPGFGVGGGIPGVAGVPSVGGVPGVGGVPGVGISPEACAAA 408
QY	421 AKAATKGCTPAAAAATAAKAAQF-----GLVPGVGVAPGVGVAPGVGVAPGLAPG 474
Dd	409 AKAATKGCTPAAAAATAAKAAQFALLNLGLVPGVGVAPGVGVAPGVGVAPGLAPG 468
QY	475 VGVAPGVGVAPGVGVAPGIPCGVAAAAATAAKAAQAQLR 515
Dd	469 VGVAPGVGVAPGVGVAPGIPCGVAAAAATAAKAAQAQLR 509
RESULT 20	
AD080527	
ID	ADE08527 standard; protein; 870 AA..
XX	AD08527;
AC	
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Novel protein (useful for identifying genetic disorders) #682.
DE	novel gene; novel protein; tissue marker; molecular weight marker;
KW	chromosome marker; genetic disorder
XW	

Db	26	-----VPGGVADAAAAYKAAKAGAGLGGVPGVGGGLGVSGAVVPPQCGAGVKPKVPGVGL	80
Qy	121	PGVYPG-GVLPGLARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGFGPQPGVPLG	179
Db	81	PGVYPGFAGVPGARFPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGFGPQPGVPLG	140
Qy	180	YPTKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPDQAAAAAATAKAAK	239
Db	141	YPIKAPKLPGGYGLPYTTGKLPYGYGPGGVA-AAGKAGYPTGTGVPDQAAAAAATAKAAK	199
Qy	240	FGAGAA--GVLPVGGAGVPGVPCALPITGGIAGVGTTPAAAATAAAAAATAKAAKAGLV	297
Db	200	FGAGAAFGAVPGVGGAGVPGVPCALPITGGIAGVGTTPAAAATAAAAAATAKAAKAGLV	259
Qy	298	PGGFGPGGVVPGAG-VPGVGVPGGAGIPVPCAGIPGAAPGVSPAAAAATAKAAKAAK	356
Db	260	PGGFGPGGVVPGFAGVPGVPGGAGIPVPCAGIPGAAGFAGVSPAAAAATAKAAKAAK	319
Qy	357	YGARPVGVGIGIPITYGVGAGFGPGFVGVGIGIPGVAGVPSVGGVPGVPGVGVGISPEAQ	416
Db	320	YGARPVGVGIGIPITYGVGAGFGPGFVGVGIGIPGVAGVPSVGGVPGVPGVGVGISPEAQ	379
Qy	417	AAAAAATAKAAKYGVTTPAAAAATAKAAKAAQFGLVPGVGVAPGVGVPVAGVGLAPGVG	476
Db	380	AAAAAATAKAAKYGVTTPAAAAATAKAAKAAQFGLVPGVGVAPGVGVPVAGVGLAPGVG	439
Qy	477	VAPGVGVAPGVGVAPGIPGPGGVAAAAATAKAAKAAQAQLR	515
Db	440	VAPGVGVAPGVGVAPGIPGPGGVAAAAATAKAAKAAQAQLR	478
RESULT 22			
ADMO3792			
ID	ADMO3792	standard; protein; 663 AA.	
XX	ADMO3792;		
AC			
XX	20-MAY-2004	(first entry)	
DT			
XX	Human protein of the invention SEQ ID NO:2477.		
DE			
XX	human; gene therapy; diagnostic marker; pharmaceutical.		
KW			
XX	Homo sapiens.		
OS			
XX	EP1347046-A1.		
PN			
XX	24-SEP-2003.		
PD			
XX	12-APR-2002; 2002EP-00008400.		
PF			
XX	22-MAR-2002; 2002JP-00137785.		
PR			
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.		
PA			
XX	Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;		
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;		
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;		
XX	WPI: 2003-723558/69.		
DR	N-PSDB; ADM01349.		
DR			
XX	New polynucleotides and polypeptides are useful in gene therapy, for		
PT	developing a diagnostic marker or medicines for regulating their		
PT	expression and activity, or as a target of gene therapy.		
XX	Claim 1; SEQ ID NO 2477; 305pp; English.		
PS			
XX	The invention relates to a novel human polynucleotide and the encoded		
CC	polypeptide. A polynucleotide of the invention may have a use in gene		
CC	therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful		
CC	as a primer for synthesizing the polynucleotide or as a probe for		

CC detecting the polynucleotide. The polynucleotides ADM031316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC protein sequence of the invention.  
XX  
SQ Sequence 663 AA;  
  
Query Match 86.1%; Score 2306.5; DB 7; Length 663;  
Best Local Similarity 87.8%; Pred. No. 1.6e-130;  
Matches 452; Conservative 0; Mismatches 2; Indels 61; Gaps 2;  
  
QY 1 GGVPGAIPGGVPGGVYFPGAGLGGALGGGKPLKPVPGGLAGAGLGAFFPAVT 60  
Db |||||||  
QY 27 GGVPGAIPGGVPGGVYFPGAGLGGALGGGKPLKPVPGGLAGAGLGG 76  
Db |||||||  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPGAGVKPKVPGVL 120  
Db |||||||  
QY 77 -----AGLGGVPGVGGVGSAGAVVPGAGVKPKVPGVL 115  
Db |||||||  
QY 121 PGVTPGVLPGARFPVPGVGLPGVPTAGVKPKAGVGAFAAGIPGVPGPQGVPLGY 180  
Db |||||||  
QY 116 PGVTPGVLPGARFPVPGVGLPGVPTAGVKPKAGVGAFAAGIPGVPGPQGVPLGY 175  
Db |||||||  
QY 181 PIKAPKLPGGVGLPYTTGKLPYGVPGVGAAGKAGYPTGTGVPQAAAAAKAAKF 240  
Db |||||||  
QY 176 PIKAPKLPGGVGLPYTTGKLPYGVPGVGAAGKAGYPTGTGVPQAAAAAKAAKF 235  
Db |||||||  
QY 241 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTTPAAAAAATAAAGAGLVPGG 300  
Db |||||||  
QY 236 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTTPAAAAAATAAAGAGLVPGG 295  
Db |||||||  
QY 301 PGFPGVVGVPAGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPVGAAGKAAKAYGAR 360  
Db |||||||  
QY 296 PGFPGVVGVPAGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPVGAAGKAAKAYGAR 355  
Db |||||||  
QY 361 PGVGVGGIPTYGVGAGGFPFGVGVGIPGVAGVSPVGGVPGVGGVSPVGAAGKAAKAYGAR 420  
Db |||||||  
QY 356 PGVGVGGIPTYGVGAGGFPFGVGVGIPGVAGVSPVGGVPGVGGVSPVGAAGKAAKAYGAR 415  
Db |||||||  
QY 421 AKAAYGVGTTPAAAAAATAAAGAGLVPGVPGVAGVPGVAGVPGVGLAPGVGVAPG 480  
Db |||||||  
QY 416 AKAAYGVGTTPAAAAAATAAAGAGLVPGVPGVAGVPGVAGVPGVGLAPGVGVAPG 445  
Db |||||||  
QY 481 VGAVPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515  
Db |||||||  
QY 446 VGAVPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 480  
Db |||||||  
  
RESULT 23  
ADB64761  
ID ADB64761 standard; protein; 617 AA.  
XX AC ADB64761;  
XX  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human protein encoded by clone NT2RP70003110.  
XX  
KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;  
KW cell regeneration; membrane protein; signal transduction-related protein;  
KW transcription-related protein; osteoporosis; neurological disease;  
KW cancer; tumour.  
XX  
OS Homo sapiens.  
XX  
XX EPI308459-A2.  
XX  
XX  
PD 07-MAY-2003.  
XX  
XX  
XX 28-MAR-2002; 2002EP-00007401.  
XX

PR 05-NOV-2001; 2001JP-00379298.  
PR 25-JAN-2002; 2002US-00350978.  
XX  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX  
DR WPI; 2003-450961/43.  
DR N-PSDB; ADB62791.  
XX  
PT New polynucleotides and polypeptides, useful for developing a diagnostic  
PT marker or medicines for regulation of their expression and activity, or  
PT as targets of gene therapy.  
XX  
PS Claim 1; Page; 222pp; English.  
XX  
CC The invention discloses a polynucleotide comprising a sequence selected  
CC from 1970 fully defined nucleotide sequences which encode novel  
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
CC or its partial peptide, an antibody binding to the polypeptide or peptide  
CC of the polynucleotide, immunologically assaying the polypeptide or  
CC peptide of the polynucleotide by contacting the polypeptide or peptide  
CC with the antibody of the encoded protein, and observing the binding  
CC between the two, a transformant carrying the polynucleotide in an  
CC expressible manner and an antisense polynucleotide. The oligonucleotide  
CC is useful as a primer for synthesising the polynucleotide, or as a probe  
CC for detecting the polynucleotide. The polynucleotides and encoded  
CC proteins are useful as pharmaceutical agents and many disease-related  
CC genes may be included in them, for developing a diagnostic marker or  
CC medicines for regulation of their expression and activity, or as targets  
CC of gene therapy. The genes are involved in tissue and/or cell  
CC regeneration. Membrane proteins, signal transduction-related proteins,  
CC transcription-related proteins, disease-related proteins and genes  
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate  
CC the activity or expression of the encoded protein to treat diseases. The  
CC sequence presented is a protein of the invention. Note: Some of the  
CC sequence data for this patent is not represented in the printed  
CC specification, but is based on sequence information supplied by the  
CC European Patent Office.  
XX  
SQ Sequence 617 AA;

Query Match 79.5%; Score 2129.5; DB 7; Length 617;  
Best Local Similarity 82.5%; Pred. No. 6.2e-120;  
Matches 425; Conservative 0; Mismatches 1; Indels 89; Gaps 4;  
  
QY 1 GGVPGAIPGGVPGGVYFPGAGLGGALGGGKPLKPVPGGLAGAGLGAFFPAVT 60  
Db |||||||  
QY 27 GGVPGAIPGGVPGGVYFPGAGLGGALGGGKPLKPVPGGLAGAGLGAFFPAVT 76  
Db |||||||  
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPGAGVKPKVPGVL 120  
Db |||||||  
QY 77 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPGAGVKPKVPGVL 136  
Db |||||||  
QY 121 PGVTPGVLPGARFPVPGVGLPGVPTAGVKPKAGVGAFAAGIPGVPGPQGVPLGY 180  
Db |||||||  
QY 137 PGVTPGVGLPYTTGKLPYGVPGVGAAGKAGYPTGTGVPQAAAAAKAAKF 240  
Db |||||||  
QY 181 PIKAPKLPGGVGLPYTTGKLPYGVPGVGAAGKAGYPTGTGVPQAAAAAKAAKF 222  
Db |||||||  
QY 163 PIKAPKLPGGVGLPYTTGKLPYGVPGVGAAGKAGYPTGTGVPQAAAAAKAAKF 300  
Db |||||||  
QY 241 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTTPAAAAAATAAAGAGLVPGG 282  
Db |||||||  
QY 223 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTTPAAAAAATAAAGAGLVPGG 360  
Db |||||||  
QY 301 PGFPGVVGVPAGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPVGAAGKAAKAYGAR 342  
Db |||||||  
QY 283 PGFPGVVGVPAGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPVGAAGKAAKAYGAR 360  
Db |||||||



PN EP1067182-A2.  
 XX 10-JAN-2001.  
 XX 07-JUL-2000; 2000EP-00114090.  
 PF 08-JUL-1999; 99JP-00194179.  
 PR 11-JAN-2000; 2000JP-00118775.  
 PR 02-MAY-2000; 2000JP-00183766.  
 XX (HELI-) HELIX RES INST.  
 PA Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 PI WPI; 2001-093989/11.  
 XX N-PSDB; AAF93849.  
 XX  
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development.  
 PS Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.  
 XX  
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAB88317  
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene  
 CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA)). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes  
 XX  
 SQ Sequence 472 AA;  
 Query Match 49.0%; Score 1314; DB 4; Length 472;  
 Best Local Similarity 55.1%; Pred. No. 3.7e-71;  
 Matches 284; Conservative 3; Mismatches 2; Indels 226; Gaps 5;  
 QY 1 GGVPGAIPGGVPGGVFPYAGALGGALGCGKELKVPVPGLAGAGLGAFFAVT 60  
 Db |||||  
 27 GGVPGAIPGGVPGGVFPYAGALGGALGCGKELKVPVPGLAGAGLGA----- 81  
 QY 61 FPGALVPGGVADAAAYKAAKACAGLGGVPGVGGVSGAVVPPGAGKVGKPGVGL 120  
 Db |||||  
 82 -----LGGVGI----- 87  
 QY 121 PGVYGVLPGARFPGVGVLPVPTGAGVKPKAPGVGGAFAGIPGVPGPGQVPLGY 180  
 Db -----  
 88 ----- 87  
 QY 181 PIKAPLPGVGLPVTGKLPYGVPGGVAGAGKAGYPTGTGVPQAAAAAATAAKF 240  
 Db |||||  
 88 -----PGVVGA-----GP----- 96  
 QY 241 GAGAGVLPVGGAGVPGVPGVGAIPGIGGIAGVGTAAAAAATAAKYGAAGLVPGG 300  
 Db |||||  
 97 -----AAAAAATAAKYGAAGLVPGG 119  
 QY 301 PGFPGVGVPGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 360

Db 120 PGFPGVGVPGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 179  
 QY 361 PGVGVGGIPTYGVGAGGPGFPGVGGIPGVAGVPSVGGVPGVGGVPGVGGISPEAAAA 420  
 Db 180 PGVGVGGIPTYGVGAGGPGFPGVGGIPGVAGVPSVGGVPGVGGVPGVGGISPEAAAA 239  
 QY 421 AKAAKYGVGTAAAAAATAAKAAQFGLVPGVPGVPGVPGVPGVPGVPGVPGVPGV 480  
 Db 240 AKAAKY-----GLVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 280  
 QY 481 VCVAPGVGVAGVPGVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515  
 Db 281 VGVAPGVGVAGVPGVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 315  
 RESULT 26  
 AAY31682  
 ID AAY31682 standard; protein; 745 AA.  
 XX  
 AC AAY31682;  
 XX  
 DT 22-NOV-1999 (first entry)  
 XX  
 DE Alanine-containing elastomer, polymer IV.  
 XX  
 KW Elastomer; bioelastomer; polymer IV; tissue augmentation;  
 KW tissue restoration; tissue reconstruction; tissue repair; implant;  
 KW fibronectin cell attachment site.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9943271-A1.  
 XX  
 PD 02-SEP-1999.  
 XX  
 PF 26-FEB-1999; 99WO-US004440.  
 XX  
 PR 27-FEB-1998; 98US-0076297P.  
 PR 29-MAY-1998; 98US-0087155P.  
 XX  
 PA (BIOE-) BIOELASTICS RES LTD.  
 XX  
 PI Urry DW, Parker TM, Glazer PA;  
 XX  
 DR WPI; 1999-540487/45.  
 XX  
 PT Augmentation or restoration of mammalian tissue by injecting solution of  
 PT peptide polymer, used for soft or hard tissue reconstruction, especially  
 PT of intervertebral disks.  
 XX  
 PS Claim 73; Page 106-109; 133pp; English.  
 XX  
 CC The present sequence represents novel alanine-containing polymer IV that  
 CC has bioelastic properties. The invention provides a method of tissue  
 CC augmentation by injecting a polymer comprising repeating peptide  
 CC monomeric units selected from nonapeptide, pentapeptide and tetrapeptide  
 CC separated by dynamic bridging segments. The polymer has an inverse  
 CC temperature transition value (Tt) that is less than the tissue  
 CC temperature, and is injected in water solution at coacervate  
 CC concentration. The polymer is injected at periurethral or subdermal sites  
 CC (for treatment of urinary incontinence or for cosmetic purposes), or into  
 CC hard or soft tissue, e.g. for repair of traumatic injury. A specific  
 CC application is restoration of intervertebral discs. Polymer IV has a Tt  
 CC value of 28 deg  
 XX  
 SQ Sequence 745 AA;  
 Query Match 34.0%; Score 911.5; DB 2; Length 745;  
 Best Local Similarity 44.8%; Pred. No. 7.2e-47;  
 Matches 265; Conservative 30; Mismatches 182; Indels 115; Gaps 40;









